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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 22:23:06 ; Search time 611 Seconds
(without alignments)
7097.342 Million cell updates/sec

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Perfect score: 729
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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 5537552 seqs, 2974263231 residues

Word size : 0
Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*
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22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------|
| 1 | 729 | 100.0 | 729 | 14 | US-10-060-585-1 |
| 2 | 729 | 100.0 | 729 | 18 | US-10-334-235-1 |
| 3 | 729 | 100.0 | 729 | 19 | US-10-787-881A-1 |
| 4 | 678 | 93.0 | 1807 | 14 | US-10-060-585-2 |
| 5 | 678 | 93.0 | 1807 | 19 | US-10-334-235-2 |
| 6 | 678 | 93.0 | 1807 | 19 | US-10-787-881A-2 |
| 7 | 675 | 92.6 | 1467 | 14 | US-10-060-585-3 |
| 8 | 675 | 92.6 | 1467 | 18 | US-10-334-235-3 |
| 9 | 675 | 92.6 | 1467 | 19 | US-10-787-881A-3 |
| 10 | 576 | 79.0 | 1518 | 14 | US-10-104-522-5 |
| 11 | 576 | 79.0 | 1518 | 14 | US-10-060-585-5 |

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| 12 | 576 | 79.0 | 1518 | 18 | US-10-334-235-5 | Sequence 5, Appli |
| 13 | 576 | 79.0 | 1518 | 18 | US-10-787-881A-5 | Sequence 5, Appli |
| 14 | 569 | 78.1 | 9100 | 19 | US-10-334-235-16 | Sequence 16, Appli |
| 15 | 551 | 75.6 | 2090 | 14 | US-10-104-522-6 | Sequence 6, Appli |
| 16 | 551 | 75.6 | 2090 | 14 | US-10-060-585-6 | Sequence 6, Appli |
| 17 | 551 | 75.6 | 2090 | 18 | US-10-334-235-6 | Sequence 6, Appli |
| 18 | 551 | 75.6 | 2090 | 19 | US-10-787-881A-6 | Sequence 6, Appli |
| 19 | 138 | 18.9 | 723 | 18 | US-10-405-123-2 | Sequence 2, Appli |
| 20 | 62 | 8.5 | 318 | 14 | US-10-252-678-3 | Sequence 3, Appli |
| 21 | 62 | 8.5 | 318 | 16 | US-10-428-662-9 | Sequence 9, Appli |
| 22 | 59 | 8.1 | 714 | 8 | US-08-940-544-4 | Sequence 4, Appli |
| 23 | 59 | 8.1 | 714 | 15 | US-10-075-947A-2 | Sequence 2, Appli |
| 24 | 59 | 8.1 | 1173 | 15 | US-10-075-947A-4 | Sequence 4, Appli |
| 25 | 56 | 7.7 | 351 | 16 | US-10-094-097B-198 | Sequence 198, App |
| 26 | 52 | 7.1 | 372 | 13 | US-10-007-790-1 | Sequence 1, Appli |
| 27 | 52 | 7.1 | 405 | 10 | US-09-726-258-36 | Sequence 36, Appli |
| 28 | 52 | 7.1 | 408 | 18 | US-10-768-193-9 | Sequence 9, Appli |
| 29 | 52 | 7.1 | 762 | 10 | US-09-726-258-43 | Sequence 43, Appli |
| 30 | 52 | 7.1 | 910 | 14 | US-10-104-522-1 | Sequence 1, Appli |
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| 32 | 51 | 7.0 | 324 | 19 | US-10-488-673-5 | Sequence 5, Appli |
| 33 | 51 | 7.0 | 324 | 19 | US-10-879-994-105 | Sequence 105, App |
| 34 | 51 | 7.0 | 351 | 18 | US-10-816-938-9 | Sequence 9, Appli |
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| 39 | 50 | 6.9 | 405 | 17 | US-10-389-417-59 | Sequence 59, Appli |
| 40 | 50 | 6.9 | 405 | 17 | US-10-452-357-68 | Sequence 68, Appli |
| 41 | 50 | 6.9 | 426 | 9 | US-09-772-120-7 | Sequence 7, Appli |
| 42 | 50 | 6.9 | 1135 | 10 | US-09-203-358-2 | Sequence 2, Appli |
| 43 | 50 | 6.9 | 1314 | 9 | US-09-903-327A-5 | Sequence 5, Appli |
| 44 | 50 | 6.9 | 1516 | 9 | US-09-903-327A-1 | Sequence 1, Appli |
| 45 | 49 | 6.7 | 366 | 17 | US-10-372-481-18 | Sequence 18, Appli |

ALIGNMENTS

RESULT 1
US-10-060-585-1
; Sequence 1, Application US/10060585
; Publication No. US20030083290A1
; GENERAL INFORMATION:
; APPLICANT: Kingsman, Alan J.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: DY0U23.001CPI
; CURRENT APPLICATION NUMBER: US/10/060,585
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 09/445375
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: GB 9711579.4
; PRIOR FILING DATE: 1997-06-04
; PRIOR APPLICATION NUMBER: GB 9713150.2
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: GB 9714230.1
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/GB99/03859
; PRIOR FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: 5T4 scFv
US-10-060-585-1

Query Match      100.0%; Score 729; DB 14; Length 729;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGTCAGCTTCAGCAGCTGCGACCTGACCTGCTGGTGAAGCCCTGGGGCTTCAGTGAAGATA 60
DB 1 GAGGTCAGCTTCAGCAGCTGCGACCTGACCTGCTGGTGAAGCCCTGGGGCTTCAGTGAAGATA 60

QY 61 TCCTGCAAGGCTTCCTGGTTACTCATCTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
DB 61 TCCTGCAAGGCTTCCTGGTTACTCATCTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

QY 121 CATGGAAGAGCCTTGAGTGAATGGAGCTTAATTAATCTTAACAATGGTGTACTCTCTAC 180
DB 121 CATGGAAGAGCCTTGAGTGAATGGAGCTTAATTAATCTTAACAATGGTGTACTCTCTAC 180

QY 181 AACAGAAATTCAGAGCAAGGCCATATTAATCTGTAGACAAAGTCAATCCACACAGCCTAC 240
DB 181 AACAGAAATTCAGAGCAAGGCCATATTAATCTGTAGACAAAGTCAATCCACACAGCCTAC 240

QY 241 ATGAGCTCCGAGCCTGACATCTGAGGCTCTGAGGCTCTATTAATCTGTGCAAGATCTACT 300
DB 241 ATGAGCTCCGAGCCTGACATCTGAGGCTCTGAGGCTCTATTAATCTGTGCAAGATCTACT 300

QY 301 ATGATTAGCAATATGTTATGAGCTACTGAGGCTCAAGTAACTCACTGACCTGCTCTCA 360
DB 301 ATGATTAGCAATATGTTATGAGCTACTGAGGCTCAAGTAACTCACTGACCTGCTCTCA 360

QY 361 GGTGCTGAGGAGCGGTGGTGGCGGCACTGGCGGCGGATCTAGTATTGTGATGACC 420
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DB 421 CAGACTCCCAATTCCTGCTTTCAGCAGGAGCAGGCTTACCAATACCTGCAAGGCC 480

QY 481 AGTCAGAGTGTGAGTGAATGATGTTGGTACCAACAGAGCCAGGCGAGTCTCTTACA 540
DB 481 AGTCAGAGTGTGAGTGAATGATGTTGGTACCAACAGAGCCAGGCGAGTCTCTTACA 540

QY 541 CTGCTCATATCCTATACATCCAGTCCGCTACCTGAGTCCCTGATCGCTTCATTGGCAGT 600
DB 541 CTGCTCATATCCTATACATCCAGTCCGCTACCTGAGTCCCTGATCGCTTCATTGGCAGT 600

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RESULT 2
US-10-334-235-1
; Sequence 1, Application US/10334235
; Publication NO. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingsman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Eillard, Fiona
; APPLICANT: Kingsman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
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; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 53268200920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding a 5T4 scFv, designated 5T4scFv.1
US-10-334-235-1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GAGGTCAGCTTCAGCAGCTGCGACCTGACCTGCTGGTGAAGCCCTGGGGCTTCAGTGAAGATA 60

QY 61 TCCTGCAAGGCTTCCTGGTTACTCATCTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
DB 61 TCCTGCAAGGCTTCCTGGTTACTCATCTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

QY 121 CATGGAAGAGCCTTGAGTGAATGGAGCTTAATTAATCTTAACAATGGTGTACTCTCTAC 180
DB 121 CATGGAAGAGCCTTGAGTGAATGGAGCTTAATTAATCTTAACAATGGTGTACTCTCTAC 180

QY 181 AACAGAAATTCAGAGCAAGGCCATATTAATCTGTAGACAAAGTCAATCCACACAGCCTAC 240
DB 181 AACAGAAATTCAGAGCAAGGCCATATTAATCTGTAGACAAAGTCAATCCACACAGCCTAC 240

QY 241 ATGAGCTCCGAGCCTGACATCTGAGGCTCTGAGGCTCTATTAATCTGTGCAAGATCTACT 300
DB 241 ATGAGCTCCGAGCCTGACATCTGAGGCTCTGAGGCTCTATTAATCTGTGCAAGATCTACT 300

QY 301 ATGATTAGCAATATGTTATGAGCTACTGAGGCTCAAGTAACTCACTGACCTGCTCTCA 360
DB 301 ATGATTAGCAATATGTTATGAGCTACTGAGGCTCAAGTAACTCACTGACCTGCTCTCA 360

QY 361 GGTGCTGAGGAGCGGTGGTGGCGGCACTGGCGGCGGATCTAGTATTGTGATGACC 420
DB 361 GGTGCTGAGGAGCGGTGGTGGCGGCACTGGCGGCGGATCTAGTATTGTGATGACC 420

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QY 481 AGTCAGAGTGTGAGTGAATGATGTTGGTACCAACAGAGCCAGGCGAGTCTCTTACA 540
DB 481 AGTCAGAGTGTGAGTGAATGATGTTGGTACCAACAGAGCCAGGCGAGTCTCTTACA 540

QY 541 CTGCTCATATCCTATACATCCAGTCCGCTACCTGAGTCCCTGATCGCTTCATTGGCAGT 600
DB 541 CTGCTCATATCCTATACATCCAGTCCGCTACCTGAGTCCCTGATCGCTTCATTGGCAGT 600

QY 601 GGATATGGAGCGGATTCATCTTTCACATCAGCATTGTCAGGCTGAAGAGCCTGGCAGTT 660
DB 601 GGATATGGAGCGGATTCATCTTTCACATCAGCATTGTCAGGCTGAAGAGCCTGGCAGTT 660

QY 661 TATTTCTGTCAAGAGATTATTAATTCCTCCGAGTTCGGTGGAGGCCACCAAGCTGGAA 720
DB 661 TATTTCTGTCAAGAGATTATTAATTCCTCCGAGTTCGGTGGAGGCCACCAAGCTGGAA 720

QY 721 ATCAAAACGG 729
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Db      721 ATCAAACGG 729
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; Publication No. US20050032216A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: Vector
; FILE REFERENCE: 021911-000330US
; CURRENT APPLICATION NUMBER: US/10/787,881A
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/GB98/01627
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Coding sequence of 5T4scFv
US-10-787-881A-1

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Best Local Similarity 100.0%; Pred. No. 0;
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QY      181 AACCAGAAATTCAGGACAAGGCCATATTAATCTGTAGACAAGTCAATCCACACAGCCTAC 240
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Db      |||||||
QY      301 ATGATTACGAATATGTTATGAGCTACTGGGGTCAAGTAACTCAGTCAACGCTCCCTCA 360
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QY      301 ATGATTACGAATATGTTATGAGCTACTGGGGTCAAGTAACTCAGTCAACGCTCCCTCA 360
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Db      |||||||
QY      361 GGTGGTGGTGGAGCGGTGGTGGCGGCATCTGGCGCGCGGATCTAGTATTGTGATGACC 420
Db      |||||||
QY      421 CAGACTCCCACTTCCTGCTGTTTTCAGCAGAGACAGGGTTACCAATACCTGCAAGGCC 480
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QY      421 CAGACTCCCACTTCCTGCTGTTTTCAGCAGAGACAGGGTTACCAATACCTGCAAGGCC 480
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Db      |||||||
QY      721 ATCAAACGG 729
Db      |||||||

RESULT 4
US-10-060-585-2
; Sequence 2, Application US/10060585
; Publication No. US20030083290A1
; GENERAL INFORMATION:
; APPLICANT: Kingsman, Alan J.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: DY0U23.001CPI
; CURRENT APPLICATION NUMBER: US/10/060,585
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 09/445375
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: GB 9711579.4
; PRIOR FILING DATE: 1997-06-04
; PRIOR APPLICATION NUMBER: GB 9713150.2
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/GB99/03859
; PRIOR FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5T4Sab1
US-10-060-585-2

Query Match      93.0%; Score 678; DB 14; Length 1807;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAGGTCCAGCTTCAGCAGTTCGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
Db      |||||||
QY      69 GAGGTCCAGCTTCAGCAGTTCGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128
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QY      129 TCCTGCAAGGCTTCCTGGTTACTCTTCACTGGCTACTACATGCATCGGTGAAGCAGAGC 188
Db      |||||||
QY      121 CATGGAAGAGCCTTCAGTGGATTGAGCTATTAATCTTAACAATGGTGTACTCTCTAC 180
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QY      189 CATGGAAGAGCCTTCAGTGGATTGAGCTATTAATCTTAACAATGGTGTACTCTCTAC 248
Db      |||||||
QY      181 AACCAGAAATTCAGGACAAGGCCATATTAATCTGTAGACAAGTCAATCCACACAGCCTAC 240
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QY      249 AACCAGAAATTCAGGACAAGGCCATATTAATCTGTAGACAAGTCAATCCACACAGCCTAC 308
Db      |||||||
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; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence encoding 574 single chain antibody
US-10-787-881A-2

Query Match 93.0%; Score 678; DB 19; Length 1807;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB |||||
QY 69 GAGGTCACAGCTTCAGCAGCTCGAGCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128
DB |||||
QY 61 TCCTGCAAGGCTTCCTGGTTACTCATTTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
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QY 129 TCCTGCAAGGCTTCCTGGTTACTCATTTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188
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QY 121 CATGCAAGAGCTTCGAGTGGATTGGAGCTATTATTAATCTTAACAATGGTTACTCTCTAC 180
DB |||||
QY 189 CATGCAAGAGCTTCGAGTGGATTGGAGCTATTATTAATCTTAACAATGGTTACTCTCTAC 248
DB |||||
QY 181 AACCAAGAAATTCAGGACAAGGCCATATTAACTGTAGACAAGTCAATCAACACAGCCTAC 240
DB |||||
QY 249 AACCAAGAAATTCAGGACAAGGCCATATTAACTGTAGACAAGTCAATCAACACAGCCTAC 308
DB |||||
QY 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGCTCTATTACTGTGCAAGATCTACT 300
DB |||||
QY 309 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGCTCTATTACTGTGCAAGATCTACT 368
DB |||||
QY 301 ATGATTACGAATGTTATGAGTACTGAGGCTCAAGTAACCTCAGTCACCGTCTCTCTCA 360
DB |||||
QY 369 ATGATTACGAATGTTATGAGTACTGAGGCTCAAGTAACCTCAGTCACCGTCTCTCTCA 428
DB |||||
QY 361 GGTGGTGGTGGAGCGGTGGTGGCGGCACTGGCGGGGAGTCTAGTATTGTGATGACC 420
DB |||||
QY 429 GGTGGTGGTGGAGCGGTGGTGGCGGCACTGGCGGGGAGTCTAGTATTGTGATGACC 488
DB |||||
QY 421 CAGACTCCCACTTCCTGCTGTTTTCAGCAGAGACAGGGTTACCAATACCTGCAAGGCC 480
DB |||||
QY 489 CAGACTCCCACTTCCTGCTGTTTTCAGCAGAGACAGGGTTACCAATACCTGCAAGGCC 548
DB |||||
QY 481 AGTCAGAGTGCAGTAATGATGTAGTGTGGTACCAACAGAGGCCAGGGCAGTCTCTCTACA 540
DB |||||
QY 549 AGTCAGAGTGTGAGTAATGATGTAGTGTGGTACCAACAGAGGCCAGGGCAGTCTCTCTACA 608
DB |||||
QY 541 CTGCTCATATCTATACATCCAGTCCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
DB |||||
QY 609 CTGCTCATATCTATACATCCAGTCCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668
DB |||||
QY 601 GGATATGGACCGGATTTTCACTTTTCAACCATCAGCACTTTTCAGGGCTGAAGACCTGGCAGT 660
DB |||||
QY 669 GGATATGGACCGGATTTTCACTTTTCAACCATCAGCACTTTTCAGGGCTGAAGACCTGGCAGT 728
DB |||||
QY 661 TATTTCTGTACAGAGATTAATTTCTCTCTCGAGCTTTCGCTGGAGGCAACAGCTGGAA 720
DB |||||
QY 729 TATTTCTGTACAGAGATTAATTTCTCTCTCGAGCTTTCGCTGGAGGCAACAGCTGGAA 788
DB |||||
QY 721 ATCAAAACGG 729
DB |||||
QY 789 ATCAAAACGG 797
DB |||||
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RESULT 7
US-10-060-585-3
; Sequence 3, Application US/10060585
; Publication No. US20030083290A1
; GENERAL INFORMATION:

; APPLICANT: Kingsman, Alan J.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: DYOU23.001CPI
; CURRENT APPLICATION NUMBER: US/10/060,585
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 09/445375
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: GB 9711579.4
; PRIOR FILING DATE: 1997-06-04
; PRIOR APPLICATION NUMBER: GB 9713150.2
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: GB 9714230.1
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/GB99/03859
; PRIOR FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B7-1.5T4.1
US-10-060-585-3

Query Match 92.6%; Score 675; DB 14; Length 1467;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 725; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GAGTCCAGCTTCAGCAGCTCGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
DB |||||
QY 739 GAGTCCAGCTTCAGCAGCTCGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798
DB |||||
QY 61 TCCTGCAAGGCTTCCTGGTTACTCATTTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
DB |||||
QY 799 TCCTGCAAGGCTTCCTGGTTACTCATTTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858
DB |||||
QY 121 CATGGAAGAGCCTTCAGTGGATTGGAGCTATTAACTCTTAACAATGGTTACTCTCTAC 180
DB |||||
QY 859 CATGGAAGAGCCTTCAGTGGATTGGAGCTATTAACTCTTAACAATGGTTACTCTCTAC 918
DB |||||
QY 181 AACCAAGAAATTCAGGACAAGGCCATATTAACTGTAGACAAGTCAATCAACACAGCCTAC 240
DB |||||
QY 919 AACCAAGAAATTCAGGACAAGGCCATATTAACTGTAGACAAGTCAATCAACACAGCCTAC 978
DB |||||
QY 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGCTCAAGTAACCTCAGTCACCGTCTCTCTCA 360
DB |||||
QY 979 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGCTCAAGTAACCTCAGTCACCGTCTCTCT 1038
DB |||||
QY 301 ATGATTACGAATGTTATGAGTACTGAGGACTCTGGGCTCAAGTAACCTCAGTCACCGTCTCTCTCA 360
DB |||||
QY 1039 ATGATTACGAATGTTATGAGTACTGAGGACTCTGGGCTCAAGTAACCTCAGTCACCGTCTCTCTCA 1098
DB |||||
QY 361 GGTGGTGGTGGAGCGGTGGTGGCGGCACTGGCGGGCGGAGTCTAGTATTGTGATGACC 420
DB |||||
QY 1099 GGTGGTGGTGGAGCGGTGGTGGCGGCACTGGCGGGCGGAGTCTAGTATTGTGATGACC 1158
DB |||||
QY 421 CAGACTCCCACTTCCTGCTTGTTCAGCAGAGACAGGGTTACCAATACCTGCAAGGCC 480
DB |||||
QY 1159 CAGACTCCCACTTCCTGCTTGTTCAGCAGAGACAGGGTTACCAATACCTGCAAGGCC 1218
DB |||||
QY 481 AGTCAGAGTGTGAGTAATGATGTAGTGTGGTACCAACAGAGGCCAGGGCAGTCTCTCTACA 540
DB |||||
QY 1219 AGTCAGAGTGTGAGTAATGATGTAGTGTGGTACCAACAGAGGCCAGGGCAGTCTCTCTACA 1278
DB |||||
QY 541 CTGCTCATATCTATACATCCAGTCCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
DB |||||
```

| | | | |
|----|------|---|------|
| Db | 1279 | CTGCTCATATCCCTATATACATCAGTCGCTACGCTGGAGTCCTGATCGCTTCATTGGCAGT | 1338 |
| Qy | 601 | GGATATGGGAGCGGATTTTCACTTTTCACCATCAGCACTTTTGCAGGCTGAAGACCTTGGCAGTT | 660 |
| Db | 1339 | GGATATGGGAGCGGATTTTCACTTTTCACCATCAGCACTTTTGCAGGCTGAAGACCTTGGCAGTT | 1398 |
| Qy | 661 | TATTTCTGTGAGCAAGAGTTATATTTCTCTCCGACGTTCCGTGAGGAGCAACCAAGCTGAA | 720 |
| Db | 1399 | TATTTCTGTGAGCAAGAGTTATATTTCTCTCCGACGTTCCGTGAGGAGCAACCAAGCTGAA | 1458 |
| Qy | 721 | ATCAAA 726 | |
| Db | 1459 | ATCAAA 1464 | |

```

RESULT 8
US-10-334-235-3
; Sequence 3, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 532682000920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of B7-1.5T4.1
US-10-334-235-3

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| Query Match | 92.6%; | Score 675; | DB 18; | Length 1467; |
|-----------------------|-----------------|--|-----------|--------------|
| Best Local Similarity | 99.9%; | Pred. No. 0; | | |
| Matches 725; | Conservative 0; | Mismatches 1; | Indels 0; | Gaps 0; |
| QY | 1 | GAGGTCAGCTTCAGCAGCTTCGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA | 60 | |
| | | | | |
| DB | 739 | GAGGTCAGCTTCAGCAGCTTCGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA | 798 | |
| QY | 61 | TCCTGCAAGGCTTCTGGTTACTCATTCACCTGGCTACTACATGCACCTGGGTGAAGCAGC | 120 | |
| | | | | |
| DB | 799 | TCCTGCAAGGCTTCTGGTTACTCATTCACCTGGCTACTACATGCACCTGGGTGAAGCAGC | 858 | |
| QY | 121 | CATGGAAGAGCCTTCGAGTGGATTGACGTATTAACTCCTAACATGGTGTTACTCTCTAC | 180 | |
| | | | | |
| DB | 859 | CATGGAAGAGCCTTCGAGTGGATTGACGTATTAACTCCTAACATGGTGTTACTCTCTAC | 918 | |
| QY | 181 | AACCAGAAATTCGAAGCAAGGCCATATTAACTGTAGCAAGTCATCCACCAGCCCTAC | 240 | |
| | | | | |
| DB | 919 | AACCAGAAATTCGAAGCAAGGCCATATTAACTGTAGCAAGTCATCCACCAGCCCTAC | 978 | |
| QY | 241 | ATGGAGCTCGGAGCCTGACATCTGAGGACTCTCGCGTCTATTACTGTGCAAGATCTACT | 300 | |
| | | | | |
| DB | 979 | ATGGAGCTCGGAGCCTGACATCTGAGGACTCTCGCGTCTATTACTGTGCAAGATCTACT | 1038 | |

| | | | | |
|----|------|--------------|---|------|
| Qy | 301 | ATGATTACGAAC | TATGTTATGGACTACTGGGTCAGTAACCTCAGTCAACCGTCTCTCTCA | 360 |
| Db | 1039 | ATGATTACGAAC | TATGTTATGGACTACTGGGTCAGTAACCTCAGTCAACCGTCTCTCTCA | 1098 |
| Qy | 361 | GTTGGTGGTGGG | AGCGTGTGGGGCAGCTGGCGGGCGGATCTAGTATTGTGATGAC | 420 |
| Db | 1099 | GTTGGTGGTGGG | AGCGTGTGGGGCAGCTGGCGGGCGGATCTAGTATTGTGATGAC | 1158 |
| Qy | 421 | CAGACTCCCACT | TTCCTGCTGTTTTCAGCAGGAGACAGGGTTACCATAACCTCGCAAGGCC | 480 |
| Db | 1159 | CAGACTCCCACT | TTCCTGCTGTTTTCAGCAGGAGACAGGGTTACCATAACCTCGCAAGGCC | 1218 |
| Qy | 481 | AGTCAGAGTGTG | AGTAATGATGTAGTTGTCACACAGAGCCAGGGCAGTCTCTTACA | 540 |
| Db | 1219 | AGTCAGAGTGTG | AGTAATGATGTAGTTGTCACACAGAGCCAGGGCAGTCTCTTACA | 1278 |
| Qy | 541 | CTGCTCATATCC | TATACATCCAGTCGTCAGCTGGAGTCCCTGATCGCTTCATTGGCAGT | 600 |
| Db | 1279 | CTGCTCATATCC | TATACATCCAGTCGTCAGCTGGAGTCCCTGATCGCTTCATTGGCAGT | 1338 |
| Qy | 601 | GGATATGGGAG | CGGATTTCACTTTTCCATCAGACACTTTGCAGGCTGAAGACCTTGGCAGTT | 660 |
| Db | 1339 | GGATATGGGAG | CGGATTTCACTTTTCCATCAGACACTTTGCAGGCTGAAGACCTTGGCAGTT | 1398 |
| Qy | 661 | TATTTCTGTGTC | AGCAAGATTATAATCTCTCCGACGTTTGGTGGAGGCACCAAGCTGGAA | 720 |
| Db | 1399 | TATTTCTGTGTC | AGCAAGATTATAATCTCTCCGACGTTTGGTGGAGGCACCAAGCTGGAA | 1458 |
| Qy | 721 | ATCAAA | 726 | |
| Db | 1459 | ATCAAA | 1464 | |

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RESULT 9
US-10-787-881A-3
; Sequence 3, Application US/10787881A
; Publication No. US20050032216A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: Vector
; FILE REFERENCE: 021911-000330US
; CURRENT APPLICATION NUMBER: US/10/787,881A
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/GB98/01627
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence encoding fusion
US-10-787-881A-3

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| | Query Match | 92.6% | Score 675; | DB 19; | Length 1467; |
|----|-----------------------|--|---------------------------------|-----------|--------------|
| | Best Local Similarity | 99.9%; | Pred. No. 0; | | |
| | Matches 725; | Conservative 0; | Mismatches 1; | Indels 0; | Gaps 0; |
| Qy | 1 | GAGETCCAGCTTCAGCAGTCTGGACCTGGA | CCTGGTGAAGCCTGGGGCTTCAGTGAAGATA | 60 | |
| | | | | | |
| Db | 739 | GAGETCCAGCTTCAGCAGTCTGGACCTGGA | CCTGGTGAAGCCTGGGGCTTCAGTGAAGATA | 798 | |
| | | | | | |
| Qy | 61 | TCCTGCAAGGCTTCTGGTTACTCATTCATGGGCTACTACATGCACTGGGTGAAGCAGAGC | | 120 | |
| | | | | | |
| Db | 799 | TCCTGCAAGGCTTCTGGTTACTCATTCATGGGCTACTACATGCACTGGGTGAAGCAGAGC | | 858 | |
| | | | | | |

| | | | | |
|----|------|-------------------|---|------|
| Qy | 121 | CATCGAAAGAGCCTTGA | GTGGAGCGTATTAATCCTAACAAATGGTGTTACTCTCTAC | 180 |
| Db | 859 | CATGGAAGAGCCTTGA | TGGAGCGTATTAATCCTAACAAATGGTGTTACTCTCTAC | 918 |
| Qy | 181 | AACCAGAGAAATTCAGG | CAAGGCCATATTAACCTGTAGCAAGTCATCCACACAGAGCCTAC | 240 |
| Db | 919 | AACCAGAGAAATTCAGG | CAAGGCCATATTAACCTGTAGCAAGTCATCCACACAGAGCCTAC | 978 |
| Qy | 241 | ATGGAGCTCCGACGCC | CTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT | 300 |
| Db | 979 | ATGGAGCTCCGACGCC | CTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT | 1038 |
| Qy | 301 | ATGATTACGAACTATG | TATTGGACTACTGGGCTCAAGTAACTCAGTCAACGCTCTCTCTCA | 360 |
| Db | 1039 | ATGATTACGAACTATG | TATTGGACTACTGGGCTCAAGTAACTCAGTCAACGCTCTCTCTCA | 1098 |
| Qy | 361 | GGTGGTGGTGGGAGCG | TGGTGGCGGCACTGGCGGGCGGGAGTCTAGTATTGTGATGACC | 420 |
| Db | 1099 | GGTGGTGGTGGGAGCG | TGGTGGCGGCACTGGCGGGCGGGAGTCTAGTATTGTGATGACC | 1158 |
| Qy | 421 | CAGACTCCCACTTCTG | CTCTGTTTTCAGCAGGAGACAGGGTTACCACTGCAAGGCC | 480 |
| Db | 1159 | CAGACTCCCACTTCTG | CTCTGTTTTCAGCAGGAGACAGGGTTACCACTGCAAGGCC | 1218 |
| Qy | 481 | AGTCAGAGTGTGAGTAA | TGATGTGGTACCAACAGAAAGCCAGGCGAGTCTCCTTACA | 540 |
| Db | 1219 | AGTCAGAGTGTGAGTAA | TGATGTGGTACCAACAGAAAGCCAGGCGAGTCTCCTTACA | 1278 |
| Qy | 541 | CTGCTCATATCCTATAC | ATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT | 600 |
| Db | 1279 | CTGCTCATATCCTATAC | ATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT | 1338 |
| Qy | 601 | GGATATGGGACGGATTT | CACTTTTACCATTACAGCACTTTGCAAGGCTGAAGACCTGGCAGTT | 660 |
| Db | 1339 | GGATATGGGACGGATTT | CACTTTTACCATTACAGCACTTTGCAAGGCTGAAGACCTGGCAGTT | 1398 |
| Qy | 661 | TATTTCTGTCAGCAAG | ATTAATTTCTCCTCCGACGTTCCGTGGAGGCCAACAAGCTGGAA | 720 |
| Db | 1399 | TATTTCTGTCAGCAAG | ATTAATTTCTCCTCCGACGTTCCGTGGAGGCCAACAAGCTGGAA | 1458 |
| Qy | 721 | ATCAAA | 726 | |
| Db | 1459 | ATCAAA | 1464 | |

| | | | |
|---|------|--|------|
| QY | 541 | CTGCTCATATCTCTATATACATCCAGTCGCTACGCTGGAGTCCTCTGATCGCTTCATTCGTCAGTT | 600 |
| | | | |
| Db | 1327 | CTGCTCATATCTCTATATACATCCAGTCGCTACGCTGGAGTCCTCTGATCGCTTCATTCGTCAGTT | 1386 |
| | | | |
| QY | 601 | GGATATGGGACGGATTTTCACCTTTCACCATCAGCACATTTTGAGAGCTCAAGACCTGGCGAGTT | 660 |
| | | | |
| Db | 1387 | GGATATGGGACGGATTTTCACCTTTCACCATCAGCACATTTTGAGAGCTCAAGACCTGGCGAGTT | 1446 |
| | | | |
| QY | 661 | TATTTCTGTCAGCAAGATTATTAATTTCTCTCCGACGTTCCGTCGAGGCGACCAAGCTGGAA | 720 |
| | | | |
| Db | 1447 | TATTTCTGTCAGCAAGATTATTAATTTCTCTCCGACGTTCCGTCGAGGCGACCAAGCTGGAA | 1506 |
| | | | |
| QY | 721 | ATCAAAACGG | 729 |
| | | | |
| Db | 1507 | ATCAAAACGG | 1515 |
| | | | |
| RESULT 11 | | | |
| US-10-060-585-5 | | | |
| ; Sequence 5, Application US/10060585 | | | |
| ; Publication No. US20030083290A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Kingsman, Alan J. | | | |
| ; APPLICANT: Bebbington, Christopher R. | | | |
| ; APPLICANT: Carroll, Miles W. | | | |
| ; APPLICANT: Ellard, Fiona M. | | | |
| ; APPLICANT: Kingsman, Susan M. | | | |

```
/ APPLICANT: Myers, Kevin A.
/ TITLE OF INVENTION: VECTOR SYSTEM
/ FILE REFERENCE: DYO023.001CP1
/ CURRENT APPLICATION NUMBER: US/10/060,585
/ CURRENT FILING DATE: 2002-09-06
/ PRIOR APPLICATION NUMBER: US 09/445375
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: GB 9711579.4
/ PRIOR FILING DATE: 1997-06-04
/ PRIOR APPLICATION NUMBER: GB 9713150.2
/ PRIOR FILING DATE: 1997-06-20
/ PRIOR APPLICATION NUMBER: GB 9714230.1
/ PRIOR FILING DATE: 1997-07-04
/ PRIOR APPLICATION NUMBER: PCT/GB00/04317
/ PRIOR FILING DATE: 2000-11-13
/ PRIOR APPLICATION NUMBER: PCT/GB99/03859
/ PRIOR FILING DATE: 1999-11-18
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5
/ LENGTH: 1518
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: B7 link ScFv sequence
US-10-060-585-5

Query Match          79.0%; Score 576; DB 14; Length 1518;
Best Local Similarity 99.6%; Pred. No. 6e-294;
Matches 726; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGGTCACGCTTCAGCAGCTGACCTGACCTGAGCTGAGCCTGGGCTTCAGTGAAGATA 60
DB 787 GAGGTCACGCTTCAGCAGCTGACCTGAGCTGAGCCTGGGCTTCAGTGAAGATA 846
QY 61 TCTGCAAGGCTTCGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACT 120
DB 847 TCTGCAAGGCTTCGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACT 906
QY 121 CATGGAAGAGCCTTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 180
DB 907 CATGGAAGAGCCTTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 966
QY 181 AACAGAAATTCAGAGCAAGGCGCATATTAACCTGTAGACAAAGTCAATCCACAGCCTAC 240
DB 967 AACAGAAATTCAGAGCAAGGCGCATATTAACCTGTAGACAAAGTCAATCCACAGCCTAC 1026
QY 241 ATGGAGCTCCGAGCCTGACCTGAGGACTCTGGGCTCTATTAATCTGTGCAAGATCTACT 300
DB 1027 ATGGAGCTCCGAGCCTGACCTGAGGACTCTGGGCTCTATTAATCTGTGCAAGATCTACT 1086
QY 301 ATGATTACGAATATGTTATGAGTACTGAGGCTCAAGTAACTCAGTCAAGCTCTCTTCA 360
DB 1087 ATGATTACGAATATGTTATGAGTACTGAGGCTCAAGTAACTCAGTCAAGCTCTCTTCA 1146
QY 361 GGTGTGTGGAGCGGCTGGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGT 420
DB 1147 GGTGTGTGGAGCGGCTGGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGT 1206
QY 421 CAGACTCCACATTCCTGCTGTTTTCAGCAGAGACAGGCTTACATTAACCTGCAAGGCC 480
DB 1207 CAGACTCCACATTCCTGCTGTTTTCAGCAGAGACAGGCTTACATTAACCTGCAAGGCC 1266
QY 481 AGTCAGAGTGTGAGTAAATGATGTAGTGTGGTACCAAGAGCAGGCGAGTCTCTTACA 540
DB 1267 AGTCAGAGTGTGAGTAAATGATGTAGTGTGGTACCAAGAGCAGGCGAGTCTCTTACA 1326
QY 541 CTGCTCATATCCTATACATCCAGTCCGTAAGCTGGAGTCCCTGATCCGCTTCAATGGCAGT 600
DB 1327 CTGCTCATATCCTATACATCCAGTCCGTAAGCTGGAGTCCCTGATCCGCTTCAATGGCAGT 1386
QY 601 GGATATGGAGCGGATTTCACTTTTCCACATCAGCATTTCAGGCTGAGACCTGSCAGTT 660
DB 1387 GGATATGGAGCGGATTTCACTTTTCCACATCAGCATTTCAGGCTGAGACCTGSCAGTT 1446
QY 661 TATTTCTGTGACGAGATTAATTAATTCCTCCGAGGTTGCGTGGAGGACCAAGCTGGAA 720
DB 1447 TATTTCTGTGACGAGATTAATTAATTCCTCCGAGGTTGCGTGGAGGACCAAGCTGGAA 1506
QY 721 ATCAAAACGG 729
DB 1507 ATCAAAACGG 1515

RESULT 12
US-10-334-235-5
/ Sequence 5, Application US/10334235
/ Publication No. US20040131591A1
/ GENERAL INFORMATION:
/ APPLICANT: Oxford Biomedica (UK) Ltd.
/ APPLICANT: Kingsman, Alan
/ APPLICANT: Bebbington, Christopher
/ APPLICANT: Carroll, Miles
/ APPLICANT: Ellard, Fiona
/ APPLICANT: Kingsman, Susan
/ APPLICANT: Myers, Kevin
/ APPLICANT: Lamikandra, Abigail
/ TITLE OF INVENTION: VECTOR SYSTEM
/ FILE REFERENCE: 532682000920
/ CURRENT APPLICATION NUMBER: US/10/334,235
/ CURRENT FILING DATE: 2002-12-30
/ PRIOR APPLICATION NUMBER: US 10/060,585
/ PRIOR FILING DATE: 2002-01-29
/ PRIOR APPLICATION NUMBER: PCT/GB00/04317
/ PRIOR FILING DATE: 2000-11-13
/ PRIOR APPLICATION NUMBER: US 09/445,375
/ PRIOR FILING DATE: 1998-06-04
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5
/ LENGTH: 1518
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: B7 Link scFv sequence
US-10-334-235-5

Query Match          79.0%; Score 576; DB 18; Length 1518;
Best Local Similarity 99.6%; Pred. No. 6e-294;
Matches 726; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGGTCACGCTTCAGCAGCTGACCTGACCTGAGCTGAGCCTGGGCTTCAGTGAAGATA 60
DB 787 GAGGTCACGCTTCAGCAGCTGACCTGAGCTGAGCCTGGGCTTCAGTGAAGATA 846
QY 61 TCTGCAAGGCTTCGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACT 120
DB 847 TCTGCAAGGCTTCGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACT 906
QY 121 CATGGAAGAGCCTTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 180
DB 907 CATGGAAGAGCCTTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 966
QY 181 AACAGAAATTCAGAGCAAGGCGCATATTAACCTGTAGACAAAGTCAATCCACAGCCTAC 240
DB 967 AACAGAAATTCAGAGCAAGGCGCATATTAACCTGTAGACAAAGTCAATCCACAGCCTAC 1026
QY 241 ATGGAGCTCCGAGCCTGACCTGAGGACTCTGGGCTCTATTAATCTGTGCAAGATCTACT 300
DB 1027 ATGGAGCTCCGAGCCTGACCTGAGGACTCTGGGCTCTATTAATCTGTGCAAGATCTACT 1086
QY 301 ATGATTACGAATATGTTATGAGTACTGAGGCTCAAGTAACTCAGTCAAGCTCTCTTCA 360
DB 1087 ATGATTACGAATATGTTATGAGTACTGAGGCTCAAGTAACTCAGTCAAGCTCTCTTCA 1146
QY 361 GGTGTGTGGAGCGGCTGGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGT 420
DB 1147 GGTGTGTGGAGCGGCTGGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGT 1206
QY 421 CAGACTCCACATTCCTGCTGTTTTCAGCAGAGACAGGCTTACATTAACCTGCAAGGCC 480
DB 1207 CAGACTCCACATTCCTGCTGTTTTCAGCAGAGACAGGCTTACATTAACCTGCAAGGCC 1266
QY 481 AGTCAGAGTGTGAGTAAATGATGTAGTGTGGTACCAAGAGCAGGCGAGTCTCTTACA 540
DB 1267 AGTCAGAGTGTGAGTAAATGATGTAGTGTGGTACCAAGAGCAGGCGAGTCTCTTACA 1326
QY 541 CTGCTCATATCCTATACATCCAGTCCGTAAGCTGGAGTCCCTGATCCGCTTCAATGGCAGT 600
DB 1327 CTGCTCATATCCTATACATCCAGTCCGTAAGCTGGAGTCCCTGATCCGCTTCAATGGCAGT 1386
QY 601 GGATATGGAGCGGATTTCACTTTTCCACATCAGCATTTCAGGCTGAGACCTGSCAGTT 660
DB 1387 GGATATGGAGCGGATTTCACTTTTCCACATCAGCATTTCAGGCTGAGACCTGSCAGTT 1446
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US-10-334-235-16

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Query Match      78.1%; Score 569; DB 18; Length 9100;
Best Local Similarity 99.6%; Pred. No. 2.9e-290;
Matches 719; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGGTCACGCTTCAGCAGCTGAGCCTGACCTGAGCTGGTGAAGCCTGGGCTTCAGTGAAGATA 60
DB 3647 GAGGTCACGCTTCAGCAGCTGAGCCTGACCTGAGCTGGTGAAGCCTGGGCTTCAGTGAAGATA 3706
QY 61 TCCTGCAAGGCTTCGTTACTACTTCATCTGCTGCTACTATCATGCTGCTGGTGAAGCAGAGC 120
DB 3707 TCCTGCAAGGCTTCGTTACTACTTCATCTGCTGCTACTATCATGCTGCTGGTGAAGCAGAGC 3766
QY 121 CATGGAAGAGCCTTCAGTGGATTTGACCTATTATTCCTAACTAACTGGTGTACTCTCTAC 180
DB 3767 CATGGAAGAGCCTTCAGTGGATTTGACCTATTATTCCTAACTAACTGGTGTACTCTCTAC 3826
QY 181 AACCGAATAATCAAGGACCAAGGCCATATTAATCTGTAGACAAGTCATCCACCAAGCCTTAC 240
DB 3827 AACCGAATAATCAAGGACCAAGGCCATATTAATCTGTAGACAAGTCATCCACCAAGCCTTAC 3886
QY 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGCTTATTAATCTGTGCAAGATCTACT 300
DB 3887 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGCTTATTAATCTGTGCAAGATCTACT 3946
QY 301 ATGATTACGAACTATGTTATGACTACTCGGGGTCAAGTAACTCACTGACCTGCTCTCTCA 360
DB 3947 ATGATTACGAACTATGTTATGACTACTCGGGGTCAAGTAACTCACTGACCTGCTCTCTCA 4006
QY 361 GGTGTGTGGAGCGGTGGTGGCGGCACTGGCGGCGGAGTCTAGTATTGTGATGACC 420
DB 4007 GGTGTGTGGAGCGGTGGTGGCGGCACTGGCGGCGGAGTCTAGTATTGTGATGACC 4066
QY 421 CAGACTCCACATCTCTGCTTTTCAGCAGAGACAGGTTTACATACCTGCGAAGGCC 480
DB 4067 CAGACTCCACATCTCTGCTTTTCAGCAGAGACAGGTTTACATACCTGCGAAGGCC 4126
QY 481 AGTCAGAGTGTGAGTAATGATGTAGTGTGGTACCAAGAGCCAGGCGAGTCTCTTACA 540
DB 4127 AGTCAGAGTGTGAGTAATGATGTAGTGTGGTACCAAGAGCCAGGCGAGTCTCTTACA 4186
QY 541 CTGCTCATATCTATACATPCAGTCCGCTACGCTGAGTCCCTGATCGCTTCATTTGGCAGT 600
DB 4187 CTGCTCATATCTATACATPCAGTCCGCTACGCTGAGTCCCTGATCGCTTCATTTGGCAGT 4246
QY 601 GGATATGGACCGATTTTCACTTTCCACCATCAGCATTTTGCAGGCTGAAGCCTGGCAGTT 660
DB 4247 GGATATGGACCGATTTTCACTTTCCACCATCAGCATTTTGCAGGCTGAAGCCTGGCAGTT 4306
QY 661 TATTTCTGTGACCAAGATTATTAATTTCTCTCCGACGTTTCGGTGGAGGCCACCAAGCTGGAA 720
DB 4307 TATTTCTGTGACCAAGATTATTAATTTCTCTCCGACGTTTCGGTGGAGGCCACCAAGCTGGAA 4366
QY 721 AT 722
DB 4367 AT 4368
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RESULT 15

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US-10-104-522-6
; Sequence 6, Application US/10104522
; Publication No. US20030180041
; GENERAL INFORMATION:
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Bebbington, C.R.
; APPLICANT: Ellard, Fiona W.
; APPLICANT: Carroll, Miles W.
; TITLE OF INVENTION: VECTOR
; FILE REFERENCE: DY023.001DV1
; CURRENT APPLICATION NUMBER: US/10104,522
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/445375
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; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/GB98/01627
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: GB9711579.4
; PRIOR FILING DATE: 1997-06-04
; PRIOR APPLICATION NUMBER: GB9713150.2
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: GB9714230.1
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2090
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 574 scFv-human IgE fusion construct.
US-10-104-522-6
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Best Local Similarity 99.6%; Pred. No. 1e-280;
Matches 701; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 CAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATATCTTCAAGGCT 72
DB 81 CAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATATCTTCAAGGCT 140
QY 73 TCTGGTACTACTTACTTCTGCTACTACATGCACTGGGTGAAGCAGGCGCATGGAAAGC 132
DB 141 TCTGGTACTACTTACTTCTGCTACTACATGCACTGGGTGAAGCAGGCGCATGGAAAGC 200
QY 133 CTTCAGTGGATTGGACGCTATTAACTCTAACTAACTGGTGTACTCTCTCAACACAGAAATTC 192
DB 201 CTTCAGTGGATTGGACGCTATTAACTCTAACTAACTGGTGTACTCTCTCAACACAGAAATTC 260
QY 193 AAGGACAAAGGCGCATATTAATCTGTAGACAAGTCATCCACACAGCCTATCATGAGCTCCG 252
DB 261 AAGGACAAAGGCGCATATTAATCTGTAGACAAGTCATCCACACAGCCTATCATGAGCTCCG 320
QY 253 AGCCTGCATCTGAGGACTCTGGGCTCTATTACTGTGCAAGATCTATATGATTAACGAAC 312
DB 321 AGCCTGCATCTGAGGACTCTGGGCTCTATTACTGTGCAAGATCTATATGATTAACGAAC 380
QY 313 TATGTTATGAGTACTGGGCTCAAGTAACTCACTCACTCCGCTCTCTCAGGTGGTGGTGG 372
DB 381 TATGTTATGAGTACTGGGCTCAAGTAACTCACTCACTCCGCTCTCTCAGGTGGTGGTGG 440
QY 373 AGCGGTGGTGGGCGCACTGGGCGGCGGATCTAGTATTGTGATGACCCAGACTCCACACA 432
DB 441 AGCGGTGGTGGGCGCACTGGGCGGCGGATCTAGTATTGTGATGACCCAGACTCCACACA 500
QY 433 TTCTCTGCTTGTTCAGCAGGAGACAGGCTTACCATTAACCTGCAAGGCGAGTCAAGAGTGTG 492
DB 501 TTCTCTGCTTGTTCAGCAGGAGACAGGCTTACCATTAACCTGCAAGGCGAGTCAAGAGTGTG 560
QY 493 AGTAAATGATGTAGDTTGGTTACCAACAGAGCCAGGCGAGTCTCTACACTGCTCATATCC 552
DB 561 AGTAAATGATGTAGDTTGGTTACCAACAGAGCCAGGCGAGTCTCTACACTGCTCATATCC 620
QY 553 TATACATCCAGTCTGCTAGCTGGAGTCCCTGATGCTTCAATTGGCAGTGATGGGAGC 612
DB 621 TATACATCCAGTCTGCTAGCTGGAGTCCCTGATGCTTCAATTGGCAGTGATGGGAGC 680
QY 613 GATTTCACTTTTCACTCAGCAGCTTTTCAGGCTGAAGACCTGGCAGTATTATTTCTGTGAG 672
DB 681 GATTTCACTTTTCACTCAGCAGCTTTTCAGGCTGAAGACCTGGCAGTATTATTTCTGTGAG 740
QY 673 CAAGATTATTAATTTCTCTCCGAGCTTCGGTGGAGGCCACCAAGCT 716
DB 741 CAAGATTATTAATTTCTCTCCGAGCTTCGGTGGAGGCCACCAAGCT 784
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Search completed: March 16, 2005, 00:46:20

Job time : 615 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 20:38:45 ; Search time 3427 Seconds
(without alignments)
8097.126 Million cell updates/sec

Title: US-10-016-686-5
Perfect score: 729
Sequence: 1 gaggtccagcttcgagtc.....ccaagctggaaatcaaacgg 729

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:

1: gb_est1:
2: gb_est2:
3: gb_hc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_ges1:
9: gb_ges2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------|--------------------|
| 1 | 117 | 16.0 | 842 | 9 | BX969451 | Reverse s |
| 2 | 86 | 11.8 | 724 | 2 | BF168514 | BF168514 601775412 |
| 3 | 86 | 11.8 | 769 | 2 | BF168556 | BF168556 601775314 |
| 4 | 66 | 9.1 | 507 | 2 | BF015548 | BF015548 uy23a08.y |
| 5 | 61 | 8.4 | 594 | 2 | BE309592 | BE309592 601094848 |
| 6 | 61 | 8.4 | 883 | 3 | BF580610 | BF580610 602093730 |
| 7 | 59 | 8.1 | 638 | 8 | AZ706203 | AZ706203 RPCT-23-2 |
| 8 | 56 | 7.7 | 348 | 8 | AZ611733 | AZ611733 1M0438F15 |
| 9 | 56 | 7.7 | 635 | 8 | AZ610015 | AZ610015 1M0435N01 |
| 10 | 52 | 7.1 | 784 | 8 | BH121432 | BH121432 RPCT-24-3 |
| 11 | 47 | 6.4 | 320 | 5 | BY346210 | BY346210 BY346210 |
| 12 | 47 | 6.4 | 529 | 6 | CA577954 | CA577954 R016F08- |
| 13 | 47 | 6.4 | 598 | 4 | B1104341 | B1104341 602889919 |
| 14 | 47 | 6.4 | 607 | 1 | AV259014 | AV259014 AV259014 |
| 15 | 47 | 6.4 | 640 | 5 | BQ109114 | BQ109114 imagegc.6 |
| 16 | 47 | 6.4 | 754 | 9 | CR026392 | CR026392 Reverse s |
| 17 | 47 | 6.4 | 794 | 4 | B1150371 | B1150371 602915205 |
| 18 | 47 | 6.4 | 801 | 5 | B0946353 | B0946353 AGENCOURT |
| 19 | 47 | 6.4 | 1576 | 3 | AK007918 | AK007918 Mus muscu |
| 20 | 46 | 6.3 | 408 | 9 | BX980485 | BX980485 Forward s |
| 21 | 46 | 6.3 | 422 | 6 | CA578211 | CA578211 K0720E02 |
| 22 | 46 | 6.3 | 465 | 6 | CA578116 | CA578116 K0718G11 |
| 23 | 46 | 6.3 | 469 | 6 | CA574907 | CA574907 K0622H02- |
| 24 | 46 | 6.3 | 472 | 6 | CA578323 | CA578323 K0722B03- |

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|----|----|-----|------|---|----------|--------------------|
| 25 | 46 | 6.3 | 493 | 6 | CA572170 | CA572170 K0531B11- |
| 26 | 46 | 6.3 | 508 | 6 | CA571278 | CA571278 K0518B06- |
| 27 | 46 | 6.3 | 508 | 6 | CA577080 | CA577080 K0704C12- |
| 28 | 46 | 6.3 | 514 | 6 | CA577707 | CA577707 K0713C01- |
| 29 | 46 | 6.3 | 538 | 6 | CA578968 | CA578968 K0731A04- |
| 30 | 46 | 6.3 | 538 | 6 | CA580316 | CA580316 K0749H01- |
| 31 | 46 | 6.3 | 623 | 4 | BG964955 | BG964955 602829272 |
| 32 | 46 | 6.3 | 639 | 2 | BE371136 | BE371136 601218628 |
| 33 | 46 | 6.3 | 692 | 6 | BY707828 | BY707828 BY707828 |
| 34 | 46 | 6.3 | 1010 | 5 | BQ921928 | BQ921928 AGENCOURT |
| 35 | 46 | 6.3 | 1524 | 3 | AK007826 | AK007826 Mus muscu |
| 36 | 45 | 6.2 | 480 | 8 | AZ892554 | AZ892554 RPCT-24-1 |
| 37 | 45 | 6.2 | 509 | 8 | AZ791472 | AZ791472 2M0041H23 |
| 38 | 45 | 6.2 | 667 | 6 | BY724790 | BY724790 BY724790 |
| 39 | 45 | 6.2 | 776 | 5 | BUS17736 | BUS17736 AGENCOURT |
| 40 | 44 | 6.0 | 350 | 6 | BY794132 | BY794132 BY794132 |
| 41 | 44 | 6.0 | 356 | 5 | BY117980 | BY117980 BY117980 |
| 42 | 44 | 6.0 | 360 | 5 | BY119951 | BY119951 BY119951 |
| 43 | 44 | 6.0 | 501 | 6 | CA577443 | CA577443 K0709F01- |
| 44 | 44 | 6.0 | 501 | 6 | CA579132 | CA579132 K0733B12- |
| 45 | 44 | 6.0 | 501 | 6 | CA579461 | CA579461 K0737G06- |

ALIGNMENTS

RESULT 1
BX969451 842 bp DNA linear GSS 05-JUL-2004
LOCUS Reverse strand read from insert in 5'HPT insertion targeting and
DEFINITION chromosome engineering clone MHPN79016, genomic survey sequence.
ACCESSION BX969451
VERSION BX969451.1 GI:49700874
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 842)
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Rogers,J. and Bradley,A.
DIRECT SUBMISSION
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER
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Location/Qualifiers
source 1..842
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN79016"
/clone_lib="MHPN"

ORIGIN

Query Match 16.0%; Score 117; DB 9; Length 842;
Best Local Similarity 100.0%; Pred. No. 4.7e-51;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 CTGGTGAAGCTGGGGCTTCAGTGAAGATATCTCGAAGGCTTCGTGTTACTCATTCAC 90
DB 314 CTGGTGAAGCTGGGGCTTCAGTGAAGATATCTCGAAGGCTTCGTGTTACTCATTCAC 373
QY 91 GGCTACTACATGCACCTGGGTGAAGCAGCCATGGAAGAGCCTTGAGTGGATTGGA 147
DB 374 GGCTACTACATGCACCTGGGTGAAGCAGCCATGGAAGAGCCTTGAGTGGATTGGA 430

RESULT 2
BF168514 724 bp mRNA linear EST 30-OCT-2000
LOCUS 601775412F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017075 5',
DEFINITION mRNA sequence.
ACCESSION BF168514

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VERSION      BF168514.1  GI:11048856
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 724)
AUTHORS     NIH-MGC http://mgs.nci.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Gilbert Smith, Ph.D.
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM9265 row: h column: 04
              High quality sequence stop: 661.

FEATURES     source
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                  /organism="Mus musculus"
                  /mol_type="mRNA"
                  /strain="C2BCH II"
                  /db_xref="taxon:10090"
                  /clone="IMAGE:4017075"
                  /tissue_type="spontaneous tumor, metastatic to mammary.
                  Stem cell origin."
                  /lab_host="DH10B"
                  /clone_lib="NCI CGAP Lu29"
                  /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
                  Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
                  Library constructed by Life Technologies. Investigator
                  providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match      11.8%; Score 86; DB 2; Length 724;
Best Local Similarity 100.0%; Pred. No. 2.2e-34;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTCGAAGGCTTCGTGTACTCATTCAC 90
    |||
Db 125 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTCGAAGGCTTCGTGTACTCATTCAC 184
    |||

QY 91 GGTACTACATGCACTGGGTGAAGCA 116
    |||
Db 185 GGTACTACATGCACTGGGTGAAGCA 210
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RESULT 3
LOCUS      BF168856
DEFINITION 60175314F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017147 5',
            mRNA sequence.
ACCESSION  BF168856
VERSION     BF168856.1  GI:11049208
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   NIH-MGC http://mgs.nci.nih.gov/
AUTHORS     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Gilbert Smith, Ph.D.
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM9265 row: k column: 04
              High quality sequence stop: 678.

FEATURES     source
              Location/Qualifiers
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                  /strain="C2BCH II"
                  /db_xref="taxon:10090"
                  /clone="IMAGE:4017147"
                  /tissue_type="spontaneous tumor, metastatic to mammary.
                  Stem cell origin."
                  /lab_host="DH10B"
                  /clone_lib="NCI CGAP Lu29"
                  /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
                  Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
                  Library constructed by Life Technologies. Investigator
                  providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match      11.8%; Score 86; DB 2; Length 769;
Best Local Similarity 100.0%; Pred. No. 2.2e-34;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTCGAAGGCTTCGTGTACTCATTCAC 90
    |||
Db 129 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTCGAAGGCTTCGTGTACTCATTCAC 188
    |||

QY 91 GGTACTACATGCACTGGGTGAAGCA 116
    |||
Db 189 GGTACTACATGCACTGGGTGAAGCA 214
    |||

RESULT 4
LOCUS      BF015548
DEFINITION uy23a08.v1 NCI_CGAP Lu30 Mus musculus cDNA clone IMAGE:3660374 5',
            similar to SW:HV14_MOUSE P01758 IG HEAVY CHAIN V REGION 108A
            PRECURSOR. ; mRNA sequence.
ACCESSION  BF015548
VERSION     BF015548.1  GI:10746880
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Gilbert Smith, Ph.D.
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
              Clone distribution: Washington University Genome Sequencing Center
              found through the I.M.A.G.E. Consortium/LLNL at:
              image.llnl.gov/image/html/iresources.shtml
              MGI:1421142
              Seq primer: -40RP from Gibco
              High quality sequence stop: 456.

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                  /clone="IMAGE:3660374"

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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9265 row: k column: 04
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                  Stem cell origin."
                  /lab_host="DH10B"
                  /clone_lib="NCI CGAP Lu29"
                  /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
                  Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
                  Library constructed by Life Technologies. Investigator
                  providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match      11.8%; Score 86; DB 2; Length 769;
Best Local Similarity 100.0%; Pred. No. 2.2e-34;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTCGAAGGCTTCGTGTACTCATTCAC 90
    |||
Db 129 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTCGAAGGCTTCGTGTACTCATTCAC 188
    |||

QY 91 GGTACTACATGCACTGGGTGAAGCA 116
    |||
Db 189 GGTACTACATGCACTGGGTGAAGCA 214
    |||

RESULT 4
LOCUS      BF015548
DEFINITION uy23a08.v1 NCI_CGAP Lu30 Mus musculus cDNA clone IMAGE:3660374 5',
            similar to SW:HV14_MOUSE P01758 IG HEAVY CHAIN V REGION 108A
            PRECURSOR. ; mRNA sequence.
ACCESSION  BF015548
VERSION     BF015548.1  GI:10746880
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Gilbert Smith, Ph.D.
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
              Clone distribution: Washington University Genome Sequencing Center
              found through the I.M.A.G.E. Consortium/LLNL at:
              image.llnl.gov/image/html/iresources.shtml
              MGI:1421142
              Seq primer: -40RP from Gibco
              High quality sequence stop: 456.

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/tissue_type="tumor, metastatic to mammary"
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/clone_lib="NCI CGAP Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; transgenic model WNT-1, expression driven by
MTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.2e-23; Length 507;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 174 CATTCACTGGCTACTACATGCACTGGTGAAGCAGCCATGAAAGACCTTGATGGA 233
|||||

QY 143 TTGGAC 148
|||||
Db 234 TTGGAC 239
|||||

RESULT 5
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LOCUS 601094848F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3489635 5',
DEFINITION mRNA sequence.
ACCESSION BE309592
VERSION BE309592.1 GI:9168025
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8530 row: 0 column: 12
High quality sequence stop: 591.
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/clone="IMAGE:3489635"
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/lab_host="DH10B"
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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 6e-21; Length 594;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 TCAGCAGGAGACAGGGTTACCATACCTGCAAGGCCAGTCAGAGTGTGATGATGTA 504
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3489635"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 6e-21; Length 594;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 TCAGCAGGAGACAGGGTTACCATACCTGCAAGGCCAGTCAGAGTGTGATGATGTA 504
|||||

/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; transgenic model WNT-1, expression driven by
MTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-23; Length 507;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 CATTCACTGGCTACTACATGCACTGGTGAAGCAGCCATGAAAGACCTTGATGGA 142
|||||
Db 174 CATTCACTGGCTACTACATGCACTGGTGAAGCAGCCATGAAAGACCTTGATGGA 233
|||||

QY 143 TTGGAC 148
|||||
Db 234 TTGGAC 239
|||||

RESULT 6
BF580610 883 bp mRNA linear EST 12-DEC-2000
LOCUS 602093730F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208022 5',
DEFINITION mRNA sequence.
ACCESSION BF580610
VERSION BF580610.1 GI:111654322
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9771 row: 1 column: 07
High quality sequence stop: 639.
Location/Qualifiers
1. 883
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4208022"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 6.3e-21; Length 883;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 TCAGCAGGAGACAGGGTTACCATACCTGCAAGGCCAGTCAGAGTGTGATGATGTA 504
|||||
Db 110 TCAGCAGGAGACAGGGTTACCATACCTGCAAGGCCAGTCAGAGTGTGATGATGTA 169
|||||

QY 505 G 505
170 G 170

RESULT 7
AZ706203 638 bp DNA linear GSS 24-JAN-2001
LOCUS RPCI-23-236G24.TJ RPCI-23 Mus musculus genomic clone
DEFINITION RPCI-23-236G24, genomic survey sequence.
ACCESSION AZ706203
VERSION AZ706203.1 GI:12433429
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

```


University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0435 row: N column: 01
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends

High quality sequence stop: 635.

Location/Qualifiers
1. .635
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM043SN01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES

source

ORIGIN

Query Match 7.7%; Score 56; DB 8; Length 635;
Best Local Similarity 100.0%; Pred. No. 3e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 CTACTACATGCTGGTGAACGACGCGCCATGGAAGACCTTGAGTGGATTGGAC 148
|||||
Db 308 CTACTACATGCTGGTGAACGACGCGCCATGGAAGACCTTGAGTGGATTGGAC 363
|||||

RESULT 10

BH121432

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Other_GSSs: RPCI-24-300D2.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.choi.org). Clones may be purchased from BACPAC
Resources (http://www.choi.org/bacpac/orderingframe.html). BAC end
page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
Plate: 300 row: D column: 2
Seq primer: T7
Class: BAC ends.

FEATURES

Location/Qualifiers

1. .784

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-300D2"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"

/note="Vector: PTARBAC1; Site 1: BamHI; Site 2: BamHI;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the PTARBAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA."

ORIGIN

Query Match 7.1%; Score 52; DB 8; Length 784;
Best Local Similarity 100.0%; Pred. No. 4.3e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 TACATGCACTGGTGAACGACGCGCCATGGAAGACCTTGAGTGGATTGGAC 148
|||||
Db 452 TACATGCACTGGTGAACGACGCGCCATGGAAGACCTTGAGTGGATTGGAC 503
|||||

RESULT 11

BY346210

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY346210 320 bp mRNA linear EST 12-DEC-2002
BY346210 RIKEN full-length enriched, whole joints Mus musculus CDNA
clone L730022G23 5', mRNA sequence.

BY346210
BY346210.1 GI:26575698

EST
Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

1 (bases 1 to 320)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawai, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrowsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Iehii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL MEDLINE PUBLISHED
Nature 420, 563-573 (2002)

COMMENT
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Iehii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues
Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES
source
1. .320
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="L730022623"
/tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"

ORIGIN
Query Match 6.4%; Score 47; DB 5; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.9e-13; Indels 0; Gaps 0;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTGCAAGGCTTCTGG 77
Db 135 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTGCAAGGCTTCTGG 181

RESULT 12
CA577954
LOCUS
DEFINITION
K0716F08-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)
IMAGE:30075139 5', mRNA sequence.
ACCESSION
CA577954

CA577954.1 GI:25126345
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 529)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Aiba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)
Unpublished (2001)
Other ESTs: K0716F08-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0716 row: F column: 08
Seq primer: M13 Reverse
High quality sequence stop: 529
POLYA=No.
Location/Qualifiers
1. .529
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6Ncr"
/db_xref="niaEST:K0716F08-5N"
/db_xref="taxon:10090"
/clone="NIA:K0716F08 IMAGE:30075139"
/tissue_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)"
/dev_stage="Age approx.10 weeks old"
/lab_host="DH10B"
/clone_lib="NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)"
/note=vector: pSPOR1 (Invitrogen); Site:1: Sali; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]. Total RNAs were obtained from Drs. Dennis Taub, Pan Longo (National Institute on Aging, USA), Jonathan Keller (National Cancer Institute, USA). Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen).
5'-pGACTAGTCTAGATCGAGCGCGCCCTTTTCTTTT-3' from 0.9 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into Sali/NotI site of pSPOR1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.1 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN
Query Match 6.4%; Score 47; DB 6; Length 529;
Best Local Similarity 100.0%; Pred. No. 2e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTGCAAGGCTTCTGG 77
Db 110 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTGCAAGGCTTCTGG 156

RESULT 13
B1104341

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CTGTTGAAGCTGGGGCTTCAGTGAAGATATCTCGAAGGCTTCTGG 77
|||||
Db 137 CTGTTGAAGCTGGGGCTTCAGTGAAGATATCTCGAAGGCTTCTGG 183
|||||

RESULT 15
BQ109114
LOCUS
DEFINITION BQ109114 640 bp mRNA linear EST 16-APR-2002
imageqc_6 2001/anj21bdr81.y1 NCI_CGAP Lu29 Mus musculus cDNA clone
IMAGE:5035013 5', mRNA sequence.
ACCESSION BQ109114
VERSION BQ109114
KEYWORDS EST.
SOURCE BQ109114.1 GI:20158768
ORGANISM Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 640)
Kale,P.I., Harsch,T.J., Folta,P.A., Nelson,D.O., Sanders,C.G. and
Prange,C.K.
The I.M.A.G.E. Consortium quality control effort: clone
ressequencing for verification
Unpublished (2001)
Other ESTs: B1104341
Contact: Prange CK
The I.M.A.G.E. Consortium
Lawrence Livermore National Laboratory
Livermore, CA, USA
Email: help@image.llnl.gov
This read has been verified (found to hit its original self in the
correct orientation), as part of the I.M.A.G.E. Consortium quality
control effort. High quality sequence is defined as having 100 or
more base pairs with a phred quality value of 20 or greater, where
a sliding window of 4 base pairs with a phred quality value of 15
or greater marks the beginning and end of the sequence. For
information on obtaining this clone, please contact
info@image.llnl.gov.
Plate: L1AM11097 row: f column: 6
Seq primer: ml3rpl
High quality sequence stop: 640.

FEATURES
source
1..640
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5035013"
/tissue_type="spontaneous tumor, metastatic to mammary."
Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match 6.4%; Score 47; DB 5; Length 640;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CTGTTGAAGCTGGGGCTTCAGTGAAGATATCTCGAAGGCTTCTGG 77
|||||
Db 122 CTGTTGAAGCTGGGGCTTCAGTGAAGATATCTCGAAGGCTTCTGG 168
|||||

Search completed: March 15, 2005, 23:20:20
Job time : 3434 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 18:05:05 ; Search time 3818 Seconds
(without alignments)
9251.926 Million cell updates/sec

Title: US-10-016-686-5

Perfect score: 729

Sequence: 1 gaggtccagcttcagctc.....ccaagctggaatacaacagg 729

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_ats.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 729 | 100.0 | 729 | 6 | BD136150 Vector. 9 |
| 2 | 729 | 100.0 | 729 | 6 | AX002778 Sequence |
| 3 | 729 | 100.0 | 729 | 6 | AX149544 Sequence |
| 4 | 678 | 93.0 | 729 | 6 | BD136268 Enhanceme |
| 5 | 678 | 93.0 | 729 | 6 | AX018532 Sequence |
| 6 | 678 | 93.0 | 729 | 6 | AX018608 Sequence |
| 7 | 678 | 93.0 | 1807 | 6 | BD136151 Vector. 9 |
| 8 | 678 | 93.0 | 1807 | 6 | AX002779 Sequence |
| 9 | 675 | 92.6 | 1467 | 6 | BD136152 Vector. 9 |
| 10 | 675 | 92.6 | 1467 | 6 | AX002780 Sequence |
| 11 | 675 | 92.6 | 1467 | 6 | AX149546 Sequence |
| 12 | 576 | 79.0 | 1518 | 6 | BD136154 Vector. 9 |
| 13 | 576 | 79.0 | 1518 | 6 | AX002782 Sequence |
| 14 | 576 | 79.0 | 1518 | 6 | AX149550 Sequence |
| 15 | 551 | 75.6 | 1796 | 6 | AX149547 Sequence |
| 16 | 551 | 75.6 | 2090 | 6 | BD136155 Vector. 9 |
| 17 | 551 | 75.6 | 2090 | 6 | AX002783 Sequence |
| 18 | 551 | 75.6 | 2090 | 6 | AX149551 Sequence |
| 19 | 126 | 17.3 | 330 | 10 | AY369876 Mus muscu |

| | | | | | | |
|----|-----|------|--------|----|-----------|--------------------|
| 20 | 126 | 17.3 | 342 | 10 | AF083186 | AF083186 Mus muscu |
| 21 | 101 | 13.9 | 548 | 10 | MUSIGHVBB | DJ3201 Mus musculu |
| 22 | 101 | 13.9 | 653 | 10 | MMIGHVH9 | X02462 Mouse germl |
| 23 | 98 | 13.4 | 130805 | 2 | AC116524 | AC116524 Mus muscu |
| 24 | 98 | 13.4 | 180673 | 10 | AC073565 | AC073565 Mus muscu |
| 25 | 86 | 11.8 | 294 | 10 | AF303833 | AF303833 Mus muscu |
| 26 | 86 | 11.8 | 321 | 10 | AY172007 | AY172007 Mus muscu |
| 27 | 86 | 11.8 | 354 | 10 | MMU60461 | U60461 Mus musculu |
| 28 | 86 | 11.8 | 370 | 10 | AY436962 | AY436962 Mus muscu |
| 29 | 86 | 11.8 | 375 | 10 | AY436970 | AY436970 Mus muscu |
| 30 | 86 | 11.8 | 384 | 10 | AY639151 | AY639151 Mus muscu |
| 31 | 86 | 11.8 | 387 | 10 | AF276290 | AF276290 Mus muscu |
| 32 | 86 | 11.8 | 729 | 6 | AR027053 | AR027053 Sequence |
| 33 | 86 | 11.8 | 729 | 6 | E10362 | E10362 cDNA encodi |
| 34 | 86 | 11.8 | 729 | 6 | I31036 | I31036 Sequence 3 |
| 35 | 86 | 11.8 | 209058 | 10 | AC079181 | AC079181 Mus muscu |
| 36 | 84 | 11.5 | 202704 | 10 | AC090843 | AC090843 Mus muscu |
| 37 | 81 | 11.1 | 324 | 10 | MUSIKCVRJ | D50385 Mus musculu |
| 38 | 80 | 11.0 | 735 | 12 | AF162710 | AF162710 Synthetic |
| 39 | 77 | 10.6 | 323 | 10 | MMIGHT82 | X59206 Mouse immu |
| 40 | 74 | 10.2 | 363 | 10 | MUSAI | L48677 Mus musculu |
| 41 | 74 | 10.2 | 435 | 10 | MMABAB | X67191 M.musculus |
| 42 | 74 | 10.2 | 475 | 10 | MMABAA | X67190 M.musculus |
| 43 | 72 | 9.9 | 333 | 10 | MMU8668 | U88668 Mus musculu |
| 44 | 72 | 9.9 | 336 | 10 | AY089724 | AY089724 Mus muscu |
| 45 | 72 | 9.9 | 345 | 10 | MMU86677 | U88677 Mus musculu |

ALIGNMENTS

| RESULT 1 | BD136150 | 729 bp | DNA | linear | PAT 18-SEP-2002 |
|------------|---|--------|-----|--------|-----------------|
| LOCUS | BD136150 | | | | |
| DEFINITION | Vector. | | | | |
| ACCESSION | BD136150 | | | | |
| VERSION | BD136150.1 GI:23231095 | | | | |
| KEYWORDS | JP 2002507117-A/1. | | | | |
| SOURCE | synthetic construct | | | | |
| ORGANISM | synthetic construct | | | | |
| REFERENCE | 1 (bases 1 to 729) | | | | |
| AUTHORS | Kingsman, S.M., Bebbington, C.R., Ellard, F.M., Carroll, M.W. and Myers, K.A. | | | | |
| TITLE | Vector | | | | |
| JOURNAL | Patent: JP 2002507117-A 1 05-MAR-2002; | | | | |
| COMMENT | OXFORD BIOMEDICA LTD | | | | |
| | OS Artificial Sequence | | | | |
| | PN JP 2002507117-A/1 | | | | |
| | PD 05-MAR-2002 | | | | |
| | PR 04-JUN-1998 JP 1999501858 | | | | |
| | PR 04-JUN-1997 GB 9711579, 4, 20-JUN-1997 GB 9713150.2 PR | | | | |
| | 04-JUL-1997 GB 9714230.1 | | | | |
| | PI SUSAN MARY KINGSMAN, CHRISTOPHER ROBERT BEBBINGTON, FIONA PI | | | | |
| | MARGARET ELLARD, | | | | |
| | PI MILES WILLIAM CARROLL, KEVIN ALAN MYERS | | | | |
| | CC C12N15/85, A61K48/00 | | | | |
| | CC Description of Artificial Sequence: DNA | | | | |
| | FH Key Location/Qualifiers | | | | |
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| | FT Location/Qualifiers | | | | |
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| | /db_xref="taxon:32630" | | | | |

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LOCUS AX149544 729 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 5 from Patent WO0136486.
ACCESSION AX149544
VERSION AX149544.1 GI:14347983
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM
REFERENCE
AUTHORS Kingsman,A.O., Kingsman,S.M., Bebbington,C.R., Carroll,M.W.,
ELLARD,F.M. and Myers,K.A.
TITLE Antibodies
JOURNAL Patent: WO 0136486-A 5 25-MAY-2001;
Oxford Biomedica (UK) Limited (GB)
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Db 1 GAGTCCAGCTTCAGCAGCTCGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
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RESULT 4
BD136268 729 bp DNA linear PAT 18-SEP-2002
LOCUS BD136268
DEFINITION Enhancement of prodrug activation.
ACCESSION BD136268
VERSION BD136268.1 GI:23231213
KEYWORDS JP 2002505341-A/21.
SOURCE synthetic construct
ORGANISM
REFERENCE
AUTHORS Stratford,I.J., Patterson,A.V., Kingsman,S.M., Kan,O., Griffiths,L.
and Mitrophanous,K.
TITLE Enhancement of prodrug activation
JOURNAL Patent: JP 2002505341-A 21 19-FEB-2002;
OXFORD BIOMEDICA LTD
COMMENT
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PN JP 2002505341-A/21
PD 19-FEB-2002
PF 05-MAR-1999 JP 2000534657
PR 06-MAR-1998 GB 9804841.6,19-AUG-1998 GB 9818103.5 PR
29-JAN-1999 GB 9902081.0
PI TAN JAMES STRATFORD,ADAM VORN PATTERSON,SUSAN MARY KINGSMAN,ON
PI KAN,
PI LEIGH GRIFFITHS,KYRIACOS MITROPHANOUS
PC A61K47/48,A61K35/76,A61K38/44,A61K45/00,A61K48/00,A61P9/10, PC
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Key Location/Qualifiers
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Best Local Similarity 99.9%; Pred. No. 0;
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Db 181 AACGAGAAATTCAGGACAGGCGCATATTAATCTAGTGAAGCCTGGGGCTTCAGTGAAGATA 240
Qy 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGCTCTATTACTGTGCAAGATCTACT 300
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|----|-----|---|-----|
| Qy | 301 | ATGATTACGAACATATGTTATAGCACTACTGGGGTCAAGTAACTCAGTCAACCGTCTCTCA | 360 |
| | | | |
| Db | 301 | ATGATTACGAACATATGTTATAGCACTACTGGGGTCAAGTAACTCAGTCAACCGTCTCTCA | 360 |
| | | | |
| Qy | 361 | GGTGGTGGTGGAGCGGTGGCGGCGCACTGGCGCGCGGATCTAGTATTTGATGACC | 420 |
| | | | |
| Db | 361 | GGTGGTGGTGGAGCGGTGGCGGCGCACTGGCGCGCGGATCTAGTATTTGATGACC | 420 |
| | | | |
| Qy | 421 | CAGACTCCACATTCCTGCTTGTTTTCAGCAGGAGACAGGGTTACCATAACTCTCAAGGCC | 480 |
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| Db | 421 | CAGACTCCACATTCCTGCTTGTTTTCAGCAGGAGACAGGGTTACCATAACTCTCAAGGCC | 480 |
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| Qy | 481 | AGTCACAGTGTGAGTAATGATGTAGTTGGTACCAACAGAAAGCCAGGGCAGTCTCTACA | 540 |
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| Db | 481 | AGTCACAGTGTGAGTAATGATGTAGTTGGTACCAACAGAAAGCCAGGGCAGTCTCTACA | 540 |
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| Qy | 541 | CTGCTCATATCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT | 600 |
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| Db | 541 | CTGCTCATATCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT | 600 |
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| Qy | 601 | GGATATGGACCGATTCACATTCACATCAGCACTTTGCAGGCTGAAGACTGGCAGTT | 660 |
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| Db | 601 | GGATATGGACCGATTCACATTCACATCAGCACTTTGCAGGCTGAAGACTGGCAGTT | 660 |
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| Qy | 661 | TATTTCTGTGCAGCAAGATTATAATTTCTCTCCGACGTTTCGTTGGAGGCCACCAAGCTGGAA | 720 |
| | | | |
| Db | 661 | TATTTCTGTGCAGCAAGATTATAATTTCTCTCCGACGTTTCGTTGGAGGCCACCAAGCTGGAA | 720 |
| | | | |
| Qy | 721 | ATCAAAACGG | 729 |
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RESULT 5
 AX018532
 LOCUS
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| | Query Match | 93.0% | Score 678; | DB 6; | Length 729; |
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| QY | 61 | TCCTGCAAGGCTTCTGGTTACTCAATTCACCTGGGCTACTACATGCACCTGGGTGAAGCAGACG | 120 | | |
| Db | 61 | TCCTGCAAGGCTTCTGGTTACTCAATTCACCTGGGCTACTACATGCACCTGGGTGAAGCAGACG | 120 | | |
| QY | 121 | CATGAAAGAGCCTTGAGTGGATTGACGTAATTAATCTCTAAACAATGGTGTACTCTCTAC | 180 | | |
| Db | 121 | CATGAAAGAGCCTTGAGTGGATTGACGTAATTAATCTCTAAACAATGGTGTACTCTCTAC | 180 | | |

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| Qy | 181 | AACAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCAATCCACACGCCTAC | 240 |
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| Db | 361 | GGTGGTGGGAGCGGTGGTGGCGGCACTGGCGCGCGGATCTAGTATTGTGATGACC | 420 |
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| Qy | 601 | GGATATGGGACGGATTTCACCTTTCCACCATCAGCACTTTGCAAGCTGGAAGCCTGGCAGT | 660 |
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| ACCESSION | AX018608 | | |
| VERSION | AX018608.1 | | |
| KEYWORDS | GI:10042738 | | |
| SOURCE | synthetic construct | | |
| ORGANISM | synthetic construct | | |
| REFERENCE | other sequences; artificial sequences. | | |
| AUTHORS | 1 | | |
| TITLE | Kingsman,S.M., Mitrophanous,K., Patterson,A.V., Stratford,I.J., | | |
| JOURNAL | Griffiths,L. and Kan.O. | | |
| | Enhanced prodrug activation | | |
| | Patent: WO 9945126-A 26 10-SEP-1999; | | |
| | KINGSMAN SUSAN MARY (GB); MITROPHANOUS KYRIANOS (GB); PATTERSON | | |
| | ADAM VORN (GB); STRATFORD IAN JAMES (GB); GRIFFITHS LEIGH (GB); KAN | | |
| | ON (GB); OXFORD BIOMEDICA LTD (GB) | | |
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Query Match          93.0%; Score 678; DB 6; Length 729;
Best Local Similarity 99.9%; Pred No. 0;
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AX002779
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DEFINITION Sequence 2 from Patent WO9855607.
ACCESSION AX002779
VERSION AX002779.1 GI:9885105
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 Babbington,C.R., Carroll,M.W., Ellard,F.M., Kingsman,S.M. and
AUTHORS Myers,K.A.
TITLE
JOURNAL
Patent: WO 9855607-A 2 10-DEC-1998;
BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
ELLARD FIONA MARGARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN
ALAN (GB); OXFORD BIOMEDICA LTD (GB)
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DB 69 GAGGTCACAGCTTCAGCAGCTCGACCTGACCTGCTGGAAGCCTGGGCTTCAGTGAAGATA 128
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DB 369 ATGATTACCAACTATGTTATGACTTACCTGGGTCAAGTAACTCAGTCACCGTCTCTCA 428
QY 361 GGTGTGTGGAGCGGTGGTGGCGGCACTGGCGGCGCGGATCTAGTATTGTGATGACC 420
DB 429 GGTGTGTGGAGCGGTGGTGGCGGCACTGGCGGCGCGGATCTAGTATTGTGATGACC 488

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RESULT 9
LOCUS BD136152 1467 bp DNA linear PAT 18-SEP-2002
DEFINITION Vector.
ACCESSION BD136152
KEYWORDS BD136152.1 GI:23231097
SYNTHETIC CONSTRUCT
SOURCE JP 2002507117-A/3.
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1467)
AUTHORS Kingsman,S.M., Bebbington,C.R., Ellard,F.M., Carroll,M.W. and
Myers,K.A.
TITLE Vector
JOURNAL Patent: JP 2002507117-A 3 05-MAR-2002;
OXFORD BIOMEDICA LTD
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PN JP 2002507117-A/3
PD 05-MAR-2002
PF 04-JUN-1998 JP 1999501858
PR 04-JUN-1997 GB 9711579.4, 20-JUN-1997 GB 9713150.2 PR
PI SUSAN MARY KINGSMAN,CHRISTOPHER ROBERT BEBBINGTON,FIONA PI
MARGARET ELLARD,
PI MILES WILLIAM CARROLL,KEVIN ALAN MYERS
PC C12N15/85,A61K48/00
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Best Local Similarity 99.9%; Pred. No. 0;
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QY 61 TCCTGCAAGGCTTCGGTTACTCATCTACTGGCTACTATGCACTGCGTGGGTGAAGCAGC 120
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| Db | 1039 | ATGATTACGAATATGTTATGAGCTACTGGGCTCAAGTAACTCTAGTCACGCTCTCTCA | 1098 |
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| Db | 1099 | GGTGGTGGTGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC | 1158 |
| QY | 421 | CAGACTCCACATCTCTGCTGTTTTCAGCAGGAGACAGGGTTACCACTGCAAGGCC | 480 |
| Db | 1159 | CAGACTCCACATCTCTGCTGTTTTCAGCAGGAGACAGGGTTACCACTGCAAGGCC | 1218 |
| QY | 481 | AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAGCCAGGCGAGTCTCTTACA | 540 |
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| DEFINITION | AX002780.1 | GI:9885107 | |
| ACCESSION | AX002780.1 | GI:9885107 | |
| VERSION | AX002780.1 | GI:9885107 | |
| KEYWORDS | synthetic construct | | |
| SOURCE | synthetic construct | | |
| ORGANISM | other sequences; artificial sequences. | | |
| REFERENCE | 1 | | |
| AUTHORS | Bebbington, C.R., Carroll, M.W., Ellard, F.M., Kingsman, S.M. and Myers, K.A. | | |
| TITLE | Vector | | |
| JOURNAL | Patent: WO 9855607-A 3 10-DEC-1998; | | |
| | BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB); | | |
| | ELLARD FIONA MARGARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN | | |
| | ALAN (GB); OXFORD BIOMEDICA LTD (GB) | | |
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| Query Match 92.6%; Score 675; DB 6; Length 1467; | | | |
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| AX149546 | | | |
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| 1467 bp DNA linear PAT 08-JUN-2001 | | | |

DEFINITION Sequence 7 from Patent WO0136486.
ACCESSION AX149546
VERSION AX149546.1 GI:14347985
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ellard,F.M. and Myers,K.A.
TITLE Antibodies
JOURNAL Patent: WO 0136486-A 7 25-MAY-2001;
Oxford Biomedica (UK) Limited (GB)
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Best Local Similarity 99.9%; Pred.No. 0;
Matches 725; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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LOCUS BD136154 1518 bp DNA linear PAT 18-SEP-2002
DEFINITION Vector.
ACCESSION BD136154
VERSION BD136154.1 GI:23231099
KEYWORDS JP 2002507117-A/5.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1518)
AUTHORS Kingsman,S.M., Bebbington,C.R., Ellard,F.M., Carroll,M.W. and Myers,K.A.
TITLE Vector
JOURNAL OXFORD BIOMEDICA LTD
COMMENT Patent: JP 2002507117-A 5 05-MAR-2002;
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PD 05-MAR-2002
PF 04-JUN-1998 JP 1999501858
PR 04-JUN-1997 GB 9711579.4, 20-JUN-1997 GB 9713150.2 PR
04-JUL-1997 GB 9714230.1
PI SUSAN MARY KINGSMAN, CHRISTOPHER ROBERT BEBBINGTON, FIONA PI
MARGARET ELLARD,
PI MILES WILLIAM CARROLL, KEVIN ALAN MYERS
PC C12N15/85,A61K48/00
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LOCUS AX002782 1518 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 5 from Patent WO9855607.
ACCESSION AX002782
VERSION AX002782.1 GI:9885111
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bebbington,C.R., Carroll,M.W., Ellard,F.M., Kingsman,S.M. and Myers,K.A.
TITLE Vector
JOURNAL Patent: WO 9855607-A 5 10-DEC-1998;
BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
ELLARD FIONA MARGARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN
ALAN (GB); OXFORD BIOMEDICA LTD (GB)
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Best Local Similarity 99.6%; Pred. No. 0;
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QY 661 TATTTCTGTGACAGATTAATTAATTTCTCTCCGAGGTTGCGTGGAGGCCACCAAGCTGGAA 720
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DEFINITION Sequence 11 from Patent WO0136486.
ACCESSION AX149550
VERSION AX149550.1 GI:14347988
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kingsman,A.O., Kingsman,S.M., Bebbington,C.R., Carroll,M.W., Ellard,F.M. and Myers,K.A.
TITLE Antibodies
JOURNAL Patent: WO 0136486-A 11 25-MAY-2001;
Oxford Biomedica (UK) Limited (GB)
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DEFINITION Sequence 8 from Patent WO0136486.
ACCESSION AX149547
VERSION AX149547.1 GI:14347986
KEYWORDS
SOURCE
ORGANISM
REFERENCE
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AUTHORS Kingsman,A.O., Kingsman,S.M., Bebbington,C.R., Carroll,M.W.,
Ellard,F.M. and Myers,K.A.
TITLE Antibodies
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Oxford Biomedica (UK) Limited (GB)
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GenCore version 5.1.6
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Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqm1980s:*
- 2: Geneseqm1990s:*
- 3: Geneseqm2000s:*
- 4: Geneseqm2001as:*
- 5: Geneseqm2001bs:*
- 6: Geneseqm2002as:*
- 7: Geneseqm2002bs:*
- 8: Geneseqm2003as:*
- 9: Geneseqm2003bs:*
- 10: Geneseqm2003cs:*
- 11: Geneseqm2003ds:*
- 12: Geneseqm2004as:*
- 13: Geneseqm2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|-------|-------|--------|----|----------|--------------------|
| 1 | 729 | 100.0 | 729 | 2 | AAV80290 | Aav80290 Murine an |
| 2 | 729 | 100.0 | 729 | 4 | AAf89729 | Aaf89729 Nucleotid |
| 3 | 678 | 93.0 | 729 | 4 | AAz19786 | Aaz19786 Anti-5T4 |
| 4 | 678 | 93.0 | 729 | 2 | AAz07810 | Aaz07810 5T4 scFv |
| 5 | 678 | 93.0 | 1807 | 2 | AAV80291 | Aav80291 Anti-5T4 |
| 6 | 675 | 92.6 | 1467 | 2 | AAV80292 | Aav80292 Human B7- |
| 7 | 675 | 92.6 | 1467 | 4 | AAf89730 | Aaf89730 Nucleotid |
| 8 | 576 | 79.0 | 1518 | 2 | AAV80294 | Aav80294 B7-1/scFv |
| 9 | 576 | 79.0 | 1518 | 4 | AAf89732 | Aaf89732 Nucleotid |
| 10 | 551 | 75.6 | 1796 | 4 | AAf89733 | Aaf89733 Nucleotid |
| 11 | 551 | 75.6 | 2090 | 2 | AAV80295 | Aav80295 ScFv-IGB1 |
| 12 | 551 | 75.6 | 2090 | 4 | AAf89734 | Aaf89734 Nucleotid |
| 13 | 86 | 11.8 | 729 | 2 | AAQ73679 | Aaq73679 Fv(GP-4) |
| 14 | 86 | 11.8 | 1413 | 12 | ADM72026 | Adm72026 Chimeric |
| 15 | 66 | 9.1 | 334 | 2 | AAT43737 | Aat43737 Anti-DNA |
| 16 | 66 | 9.1 | 1401 | 9 | AAD58178 | Aad58178 Mouse vir |
| 17 | 63 | 8.6 | 906 | 2 | AAV00611 | Aav00611 Anti-huma |
| 18 | 62 | 8.5 | 318 | 2 | AAQ46080 | Aaq46080 Sequence |
| 19 | 62 | 8.5 | 318 | 2 | AAQ47059 | Aaq47059 HPI/2 VK. |
| 20 | 62 | 8.5 | 318 | 2 | AAQ67344 | Aaq67344 Anti-VLA4 |

| | | | | | | |
|----|----|-----|------|----|----------|---------------------|
| 21 | 62 | 8.5 | 318 | 2 | AAQ65623 | Aaq65623 HPI/2 lig |
| 22 | 62 | 8.5 | 318 | 2 | AAQ69193 | Aaq69193 HPI/2 VK |
| 23 | 62 | 8.5 | 318 | 2 | AAQ83571 | Aaq83571 Anti-VLA- |
| 24 | 62 | 8.5 | 318 | 2 | AAV66800 | Aav66800 Anti-VLA- |
| 25 | 62 | 8.5 | 318 | 2 | AAV02232 | Aav02232 Anti-VLA- |
| 26 | 62 | 8.5 | 318 | 2 | AAx15094 | Aax15094 cDNA enco |
| 27 | 62 | 8.5 | 318 | 2 | AAx27914 | Aax27914 Anti VLA- |
| 28 | 62 | 8.5 | 318 | 2 | AAx86185 | Aax86185 cDNA enco |
| 29 | 62 | 8.5 | 318 | 4 | AAf86602 | Aaf86602 Murine an |
| 30 | 62 | 8.5 | 318 | 8 | ABx93815 | Abx93815 Mouse ant |
| 31 | 62 | 8.5 | 318 | 9 | ACD28356 | Acd28356 cDNA enco |
| 32 | 62 | 8.5 | 318 | 10 | ADI25184 | Adi25184 Murine HP |
| 33 | 62 | 8.5 | 318 | 12 | ADF94348 | Adf94348 Mouse ant |
| 34 | 62 | 8.5 | 318 | 13 | ADR40361 | Adr40361 Anti-VLA- |
| 35 | 62 | 8.5 | 318 | 13 | ADR40279 | Adr40279 Anti-VLA- |
| 36 | 61 | 8.4 | 384 | 6 | AAD46727 | Aad46727 Chimeric |
| 37 | 61 | 8.4 | 726 | 4 | AAF30723 | Aaf30723 Anti-FIX/ |
| 38 | 61 | 8.4 | 882 | 2 | AAQ48038 | Aaq48038 Monoclon |
| 39 | 59 | 8.1 | 714 | 2 | AAf86310 | Aaf86310 Single ch |
| 40 | 59 | 8.1 | 714 | 6 | ABA92027 | Abag92027 Anti-disi |
| 41 | 59 | 8.1 | 1173 | 2 | AAf86312 | Aaf86312 Single ch |
| 42 | 56 | 7.7 | 356 | 2 | AAQ28522 | Aaq28522 Hypercalc |
| 43 | 56 | 7.7 | 357 | 10 | ABT15845 | Abt15845 Anti-huma |
| 44 | 56 | 7.7 | 405 | 2 | AAQ30754 | Aaq30754 p12-h2. 3 |
| 45 | 56 | 7.7 | 828 | 10 | ABT15854 | Abt15854 Anti-huma |

ALIGNMENTS

RESULT 1

AAV80290

ID AAV80290 standard; cDNA; 729 BP.

XX AC AAV80290;

XX DT 15-MAR-1999 (first entry)

XX DE Murine anti-5T4 antigen monoclonal antibody scFv DNA.

XX KW Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen; monoclonal antibody; single chain antibody; scFv; mouse; 5T4scFv.1; 8s.

XX OS Mus sp.

XX OS Synthetic.

XX OS Chimeric.

XX PN WO9855607-A2.

XX PD 10-DEC-1998.

XX PF 04-JUN-1998; 98WO-GB001627.

XX PR 04-JUN-1997; 97GB-00011579.

XX PR 20-JUN-1997; 97GB-00013150.

XX PA 04-JUL-1997; 97GB-00014230.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX PI Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;

XX WPI; 1999-059910/05.

XX P-PSDB; AAW86002.

XX PT New vector encoding a tumour interacting protein for treating cancer - contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat cancer.

XX Example 1; Fig 1A; 82pp; English.

XX CC This DNA sequence encodes a 5T4 scFv, designated 5T4scFv.1 (see AAW86002), comprising the heavy chain variable region (VH) from the murine 5T4 monoclonal antibody followed by a 15-amino acid flexible


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QY 61 TCCTGCAAGGCTTCGTGTTACTCATTCTGCTACTATCATGCACTGGGTGAGCAGAGC 120
DB 61 TCCTGCAAGGCTTCGTGTTACTCATTCTGCTACTATCATGCACTGGGTGAGCAGAGC 120

QY 121 CATGCAAGAGCCTTGAGTGGATTGAGTATTAATCCTAACTGGTGTACTCTCTAC 180
DB 121 CATGCAAGAGCCTTGAGTGGATTGAGTATTAATCCTAACTGGTGTACTCTCTAC 180

QY 181 AACCAAGAAATTCAGGACAAGGCCATATTAATCTGTAGACAGTATCCACCAAGCCTAC 240
DB 181 AACCAAGAAATTCAGGACAAGGCCATATTAATCTGTAGACAGTATCCACCAAGCCTAC 240

QY 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
DB 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

QY 301 ATGATTACGAATCTGTTATGAGTACTTGGGTCAAGTAACTCAGTCAAGTCTCTCTCA 360
DB 301 ATGATTACGAATCTGTTATGAGTACTTGGGTCAAGTAACTCAGTCAAGTCTCTCTCA 360

QY 361 GGTGTTGGTGGAGCGGTGGTGGCGGCACTGCGCGCGGCGATCTAGTATTGTGATGACC 420
DB 361 GGTGTTGGTGGAGCGGTGGTGGCGGCACTGCGCGCGGCGATCTAGTATTGTGATGACC 420

QY 421 CAGACTCCCACTTCTGCTGTTTTCAGCAGAGACAGGTTACCATTAACCTGCAAGGCC 480
DB 421 CAGACTCCCACTTCTGCTGTTTTCAGCAGAGACAGGTTACCATTAACCTGCAAGGCC 480

QY 481 AGTCAGAGTGTGAGTAATGATGTAGTGTGGTACCAAGAGCCAGGCGAGTCTCTTACA 540
DB 481 AGTCAGAGTGTGAGTAATGATGTAGTGTGGTACCAAGAGCCAGGCGAGTCTCTTACA 540

QY 541 CTGCTCATATCTCTATACATCCAGTCCGCTACGCTGGAGTCCCTGATCGCTTCAATGGCAGT 600
DB 541 CTGCTCATATCTCTATACATCCAGTCCGCTACGCTGGAGTCCCTGATCGCTTCAATGGCAGT 600

QY 601 GGATATGGAGCGGATTTCACTTTCAGATCAGCATCTTTCAGGCTGAGACCTGCGAGTT 660
DB 601 GGATATGGAGCGGATTTCACTTTCAGATCAGCATCTTTCAGGCTGAGACCTGCGAGTT 660

QY 661 TATTTCTGTGCAAGATTTAATATCTCTCCGAGTTCGGTGGAGGACCAAGCTGGA 720
DB 661 TATTTCTGTGCAAGATTTAATATCTCTCCGAGTTCGGTGGAGGACCAAGCTGGA 720

QY 721 ATCAAACGG 729
DB 721 ATCAAACGG 729

RESULT 3
AAZ19786
ID AAZ19786 standard; DNA; 729 BP.
XX AC AAZ19786;
XX XX
XX DT 06-DEC-1999 (first entry)
XX DE Anti-574 secreted single chain antibody Fv fragment DNA.
XX KW Cytochrome; targeting; localisation; cancer; tumour; prodrug; reduction;
XX KW nucleus; db.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX CDS 1..729
XX FT /*tag= a
XX FT /product= "Anti-574 secreted single chain antibody Fv
XX FT fragment"
XX XX
XX PN W09945127-A2.
XX XX

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PD 10-SEP-1999.
XX PF
XX PF 05-MAR-1999; 99WO-GB000674.
XX PR
XX PR 06-MAR-1998; 98GB-00004841.
XX PR 19-AUG-1998; 98GB-00018103.
XX PR 29-JAN-1999; 99GB-00002081.
XX PA
XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX PI Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;
XX PI Mitrophanous K;
XX XX
XX DR WPI; 1999-551046/46.
XX DR P-PSDB; AAY42294.
XX PT
XX PT New prodrug activating agent targeted to selected cells or tissues,
XX PT particularly hypoxic cells, for treating e.g. tumors.
XX PS
XX PS Example 9; Fig 3; 187pp; English.
XX CC
XX CC This sequence represents an example of a DNA encoding a secreted single
XX CC chain antibody Fv fragment, which is involved in transcellular
XX CC localisation. In this example, the antibody is directed against the 574
XX CC antigen. A secreted single chain antibody Fv fragment can be fused to
XX CC cytochrome P450 reductase (P450R) derivatives such as anchorless P450R
XX CC (AAY42287) or FN fragment (AAY42288). This enables the fusion protein to
XX CC be delivered to other cells where it is then transported to the nucleus.
XX CC Many drugs' sites of action are in the nucleus, rather than the
XX CC cytoplasm, where P450R normally functions. P450R or its derivatives can
XX CC be used to activate prodrugs to their active form via reduction.
XX CC Administration of a prodrug is useful where the active drug may be
XX CC metabolised before it reaches its site of action or where the active drug
XX CC is cytotoxic, e.g., anticancer drugs. Targeted delivery of such prodrug
XX CC activators allows a reduction in dose of the prodrug, and thus of
XX CC systemic side-effects. P450R derivative fusion proteins, or vectors that
XX CC express them, are specifically used to treat tumours, inflammation,
XX CC atherosclerosis and muscular dystrophy, but may also be used to treat
XX CC many other conditions, e.g., cerebral malaria, rheumatoid arthritis, or
XX CC conditions associated with hypoxia, ischaemia or hypoglycaemia, or to
XX CC deliver antibiotics, antiviral agents, analgesics, anaesthetics, anti-
XX CC inflammatory, antineoplastic agents and diagnostic agents
XX SQ
XX SQ Sequence 729 BP; 180 A; 179 C; 189 G; 181 T; 0 U; 0 Other;
XX
XX Query Match 93.0%; Score 678; DB 2; Length 729;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGCTGTAAGCCTGGGGCTTCAGTGAAGATA 60
DB 1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGCTGTAAGCCTGGGGCTTCAGTGAAGATA 60
QY 61 TCCTGCAAGGCTTCGTGTTACTCATTCTGCTACTATCATGCACTGGGTGAGCAGAGC 120
DB 61 TCCTGCAAGGCTTCGTGTTACTCATTCTGCTACTATCATGCACTGGGTGAGCAGAGC 120
QY 121 CATGCAAGAGCCTTGAGTGGATTGAGTATTAATCCTAACTGGTGTACTCTCTAC 180
DB 121 CATGCAAGAGCCTTGAGTGGATTGAGTATTAATCCTAACTGGTGTACTCTCTAC 180
QY 181 AACCAAGAAATTCAGGACAAGGCCATATTAATCTGTAGACAGTATCCACCAAGCCTAC 240
DB 181 AACCAAGAAATTCAGGACAAGGCCATATTAATCTGTAGACAGTATCCACCAAGCCTAC 240
QY 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
DB 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
QY 301 ATGATTACGAATCTGTTATGAGTACTTGGGTCAAGTAACTCAGTCAAGTCTCTCTCA 360
DB 301 ATGATTACGAATCTGTTATGAGTACTTGGGTCAAGTAACTCAGTCAAGTCTCTCTCA 360

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QY 361 GGTGGTGGGAGCGTGGTGGGCGGACCTGGCGGCGGATCTAGTATTGTGATGACC 420
 Db |||||
 QY 361 GGTGGTGGGAGCGGTGGTGGGCGGACCTGGCGGCGGATCTAGTATTGTGATGACC 420
 Db |||||
 QY 421 CAGACTCCACATCTCTGCTGTTGTTTCAGCAGGAGACAGAGGTTACCAATACCTGCAAGGCC 480
 Db |||||
 QY 421 CAGACTCCACATCTCTGCTGTTGTTTCAGCAGGAGACAGAGGTTACCAATACCTGCAAGGCC 480
 Db |||||
 QY 481 AGTCAGAGTGTAGTAAATGATGTAGTGTGGTACCAACAGAGCGGCGAGTCTCTCTACA 540
 Db |||||
 QY 481 AGTCAGAGTGTAGTAAATGATGTAGTGTGGTACCAACAGAGCGGCGAGTCTCTCTACA 540
 Db |||||
 QY 541 CTGCTCATATCTATACCTACCTAGCTGCTAGCTGGAGTCCCTGATCGCTTCAATGGCAGT 600
 Db |||||
 QY 541 CTGCTCATATCTATACCTAGCTGCTAGCTGGAGTCCCTGATCGCTTCAATGGCAGT 600
 Db |||||
 QY 601 GGATATGGACCGGATTTCACTTTCCACATCAGCACTTTTCAGGCTGAAGACCTGGCAGTT 660
 Db |||||
 QY 601 GGATATGGACCGGATTTCACTTTCCACATCAGCACTTTTCAGGCTGAAGACCTGGCAGTT 660
 Db |||||
 QY 661 TATTCTGTGACAGATTAATTAATCTCTCCGAGTTCGGTGGAGGACCAAGCTGGAA 720
 Db |||||
 QY 661 TATTCTGTGACAGATTAATTAATCTCTCCGAGTTCGGTGGAGGACCAAGCTGGAA 720
 Db |||||
 QY 721 ATCAAAACGG 729
 Db |||||
 QY 721 ATCAAAACGG 729
 Db |||||

RESULT 4

AAZ07810
 ID AAZ07810 standard; DNA; 729 BP.
 XX
 AC AAZ07810;
 XX
 DT 23-NOV-1999 (first entry)
 XX
 DE 5T4 scFv antibody encoding DNA.
 XX
 KW Prodrug; localization domain; tumor-selective antibody; cytochrome P450;
 KW prodrug activating domain; modified hematopoietic stem cell; MHC; tumor;
 KW inflammation; atherosclerosis; muscular dystrophy; cerebral malaria;
 KW rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; tumor antigen;
 KW 5T4 scFv; ss.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..729
 FT /*tag= a
 XX
 PN W09945126-A2.
 XX
 PD 10-SEP-1999.
 XX
 PF 05-MAR-1999; 99WO-GB000672.
 XX
 PR 06-MAR-1998; 98GB-00004841.
 PR 19-AUG-1998; 98GB-00018103.
 PR 29-JAN-1999; 99GB-00002081.
 XX
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 PI Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;
 PI Mitrophanous K;
 XX
 XX WPI; 1999-540852/45.
 DR P-PSDB; AAY27407.
 DR
 XX New prodrug activating agent targeted to selected cells or tissues,
 PT particularly hypoxic cells, for treating e.g. tumors or inflammation.
 XX
 PS Example 9; Fig 3F; 149pp; English.

XX
 CC The invention provides a new prodrug activating agent that comprises: (i)
 CC a localization domain (LD; other than a tumor-selective antibody) and a
 CC prodrug activating domain (PAD); (ii) at least one nucleic acid encoding
 CC a cytochrome P450 and under control of at least one constitutive or
 CC inducible expression controlling sequence or (iii) a modified hematopoietic
 CC stem cell (MHC) containing at least one nucleic acid encoding a PAD and
 CC under control of elements as in (ii). The prodrug activating agent or
 CC vectors that express them, are specifically used to treat tumors,
 CC inflammation, atherosclerosis and muscular dystrophy, but may also be
 CC used to treat many other conditions, e.g. cerebral malaria, rheumatoid
 CC arthritis, or conditions associated with hypoxia, hypoglycemia or
 CC ischemia, or to deliver antibiotics, antiviral agents, analgesics,
 CC anesthetics, anti-inflammatory, antineoplastic agents and diagnostic
 CC agents. LD optimize activity of PAD, e.g. by delivering it to selected
 CC locations or by delivering it to neighboring cells (bystander effect),
 CC and allow a reduction in dose of prodrug, and thus of systemic side-
 CC effects. Nucleic acids encoding the agent may be expressed selectively in
 CC hypoxic cells. The present sequence represents the DNA encoding the
 CC single chain variable antibody fragment against the tumor antigen 5T4
 CC (5T4 scFv). 5T4 scFv is used in the construction of a fusion protein
 CC comprising 5T4 scFv and a human P450 reductase derivative alp450R
 XX
 SQ Sequence 729 BP; 180 A; 179 C; 189 G; 181 T; 0 U; 0 Other;

Query Match 93.0%; Score 678; DB 2; Length 729;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCTGGGGCTTCAGTGAAGATA 60
 Db |||||
 QY 1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCTGGGGCTTCAGTGAAGATA 60
 Db |||||
 QY 61 TCCTGCAAGGCTTCTGGTTACTCACTGCTGCTACTACATGCTGGGTGAAGCAGAGC 120
 Db |||||
 QY 61 TCCTGCAAGGCTTCTGGTTACTCACTGCTGCTACTACATGCTGGGTGAAGCAGAGC 120
 Db |||||
 QY 121 CATGGAAGACCTTGAGTGGATGGAGCTATTAATCTTAACATGGTGTACTCTCTAC 180
 Db |||||
 QY 121 CATGGAAGACCTTGAGTGGATGGAGCTATTAATCTTAACATGGTGTACTCTCTAC 180
 Db |||||
 QY 181 AACAGAAATTCAGAGCAAGGCCATATTAATCTAGACAAAGTCAATCCACACAGCCTAC 240
 Db |||||
 QY 181 AACAGAAATTCAGAGCAAGGCCATATTAATCTAGACAAAGTCAATCCACACAGCCTAC 240
 Db |||||
 QY 241 ATGAGACTCCGACCTGACATCTGAGGACTCTGGGCTCTATTACTGTGCAAGATCTACT 300
 Db |||||
 QY 241 ATGAGACTCCGACCTGACATCTGAGGACTCTGGGCTCTATTACTGTGCAAGATCTACT 300
 Db |||||
 QY 301 ATGATTACGAACATATGTTATGGACTCTGGGCTCAAGTAACTCAGTCACCGTCTCTCA 360
 Db |||||
 QY 301 ATGATTACGAACATATGTTATGGACTCTGGGCTCAAGTAACTCAGTCACCGTCTCTCA 360
 Db |||||
 QY 361 GGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGATCTAGTATTGTGATGACC 420
 Db |||||
 QY 361 GGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGATCTAGTATTGTGATGACC 420
 Db |||||
 QY 421 CAGACTCCACATCTCTGCTTGTTCAGCAGGAGACAGGGTTACCAATACCTGCAAGGCC 480
 Db |||||
 QY 421 CAGACTCCACATCTCTGCTTGTTCAGCAGGAGACAGGGTTACCAATACCTGCAAGGCC 480
 Db |||||
 QY 481 AGTCAGAGTGTAGTAAATGATGTAGTGTGGTACCAACAGAGCGGCGAGTCTCTCTACA 540
 Db |||||
 QY 481 AGTCAGAGTGTAGTAAATGATGTAGTGTGGTACCAACAGAGCGGCGAGTCTCTCTACA 540
 Db |||||
 QY 541 CTGCTCATATCTATACCTACCTAGCTGCTAGCTGGAGTCCCTGATCGCTTCAATGGCAGT 600
 Db |||||
 QY 541 CTGCTCATATCTATACCTAGCTGCTAGCTGGAGTCCCTGATCGCTTCAATGGCAGT 600
 Db |||||
 QY 601 GGATATGGAGCGGATTTCACTTTCCACATCAGCACTTTTCAGGCTGAAGACCTGGCAGTT 660
 Db |||||
 QY 601 GGATATGGAGCGGATTTCACTTTCCACATCAGCACTTTTCAGGCTGAAGACCTGGCAGTT 660
 Db |||||

QY 661 TATTTCTGTGACGAGATTATAATTTCTCTCCGACGTTGGTGGAGGACCAAGCTGGAA 720
 Db |||||||
 661 TATTTCTGTGACGAGATTATAATTTCTCTCCGACGTTGGTGGAGGACCAAGCTGGAA 720
 QY 721 ATCAACGG 729
 Db |||||||
 721 ATCAACGG 729

RESULT 5

AAV80291
 ID AAV80291 standard; cDNA; 1807 BP.
 AC AAV80291;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Anti-5T4 single chain antibody 5T4Sabl DNA.
 XX
 KW Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
 KW monoclonal antibody; single chain antibody; mouse; human; 5T4Sabl; ss.
 XX

OS Mus sp.
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.

XX Key Location/Qualifiers
 FH CDS
 FT 3..1790
 FT /*tag= a
 XX

XX WO9855607-A2.

XX 10-DEC-1998.

XX 04-JUN-1998; 98WO-GB001627.

XX 04-JUN-1997; 97GB-00011579.

XX 20-JUN-1997; 97GB-00013150.

XX 04-JUL-1997; 97GB-00014230.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;

XX WPI; 1999-059910/05.

XX P-PSDB; AAW86003.

XX New vector encoding a tumour interacting protein for treating cancer -

XX contains a desired nucleotide sequence and/or protein which recognises

XX tumours, and is used as a gene delivery system to treat cancer.

XX Example 1; Fig 1B; 82pp; English.

XX This DNA sequence encodes a single chain antibody (Sabl), termed 5T4Sabl

XX (see AAW86003), comprising an scFv derived from murine monoclonal

XX antibody 5T4 (see AAW86002) and the human g1 constant region. It was

XX constructed from cassettes comprising a translation initiation signal and

XX signal peptide (see AAV80297), the sequence of the secreted portion of

XX 5T4scFv.1, and the sequence of the human g1 constant region genomic

XX clone. The trophoblast cell surface antigen defined by 5T4 is expressed

XX at high levels on the cells of a wide variety of human tumours. The

XX invention relates to a vector comprising a nucleotide sequence coding for

XX a tumour interacting protein (TIP) and optionally a nucleotide sequence

XX of interest (NOI) which encodes a protein of interest (POI), the vector

XX being capable of delivering the NOI and/or POI to the tumour recognised

XX by the TIP. Delivery can be in vivo or ex vivo. The vector is used to

XX treat cancer, and may also be used as a gene delivery system for introducing

XX at least 1 gene encoding a TIP (preferably a tumour binding protein) into

XX a haematopoietic cell lineage

XX Sequence 1807 BP; 432 A; 543 C; 469 G; 363 T; 0 U; 0 Other;

Query Match 93.0%; Score 678; DB 2; Length 1807;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGTCCAGCTTTCAGCAGCTCTGGACCTGACCTGGTGAAGCCCTGGGGCTTTCAGTGAAGATA 60

Db |||||||

69 GAGGTCCAGCTTTCAGCAGCTCTGGACCTGACCTGGTGAAGCCCTGGGGCTTTCAGTGAAGATA 128

QY 61 TCCTGCAAGGCTTCTGGTTACTCATTTCACTGGCTACTATGCACTGGGTGAAGCAGAGC 120

Db |||||||

129 TCCTGCAAGGCTTCTGGTTACTCATTTCACTGGCTACTATGCACTGGGTGAAGCAGAGC 188

QY 121 CATGGAAGAGCCTTGAGTGAATGGAGCTATTATCTTAACAATGGTGTACTCTCTAC 180

Db |||||||

189 CATGGAAGAGCCTTGAGTGAATGGAGCTATTATCTTAACAATGGTGTACTCTCTAC 248

QY 181 AACAGAAATTCAGGACCAAGGCCATATTAACTGTAGACAAGTCATCAACACACAGCTAC 240

Db |||||||

249 AACAGAAATTCAGGACCAAGGCCATATTAACTGTAGACAAGTCATCAACACACAGCTAC 308

QY 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGCTCTATTACTGTGCAAGATCTACT 300

Db |||||||

309 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGCTCTATTACTGTGCAAGATCTACT 368

QY 301 ATGATTACAACTATGTTATGCACTACTGGGCTCAAGTAACTCACTCACTCTCTCTCA 360

Db |||||||

369 ATGATTACAACTATGTTATGCACTACTGGGCTCAAGTAACTCACTCACTCTCTCTCA 428

QY 361 GGTGTGGTGGAGCGGTGGGGGCACTGGCGGCGGATCTAGTATTGTGATGACC 420

Db |||||||

429 GGTGTGGTGGAGCGGTGGGGGCACTGGCGGCGGATCTAGTATTGTGATGACC 488

QY 421 CAGACTCCCACTCA 480

Db |||||||

489 CAGACTCCCACTCA 548

QY 481 AGTCAGAGTGTGAGTAATGATGTAGTTGGTACCAAGAGCCAGGGCAGTCTCTCTACA 540

Db |||||||

549 AGTCAGAGTGTGAGTAATGATGTAGTTGGTACCAAGAGCCAGGGCAGTCTCTCTACA 608

QY 541 CTGCTCATATCTTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCAATTCGCACT 600

Db |||||||

609 CTGCTCATATCTTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCAATTCGCACT 668

QY 601 GGATATGGGACGGATTTTCACTTTTCACTATCAGCACTTTTGCAGGCTGAAGACCTGGCAGTT 660

Db |||||||

669 GGATATGGGACGGATTTTCACTTTTCACTATCAGCACTTTTGCAGGCTGAAGACCTGGCAGTT 728

QY 661 TATTTCTGTGCAAGATTAATTAATTTCTCTCGAGCTTGGTGGAGGCCAAGCTGGAA 720

Db |||||||

729 TATTTCTGTGCAAGATTAATTAATTTCTCTCGAGCTTGGTGGAGGCCAAGCTGGAA 788

QY 721 ATCAACGG 729

Db |||||||

789 ATCAACGG 797

RESULT 6

AAV80292

ID AAV80292 standard; cDNA; 1467 BP.

XX AC AAV80292;

XX DT 15-MAR-1999 (first entry)

XX DE Human B7-1.5T4.1 gene fusion, specific for human 5T4.

XX KW Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
 KW monoclonal antibody; single chain antibody; scFv; mouse; human; B7-1;
 KW co-stimulatory molecule; ss.

XX OS Mus sp.

OS Homo sapiens.

OS Synthetic.
OS Chimeric.
XX WO9855607-A2.
XX 10-DEC-1998.
XX 04-JUN-1998; 98WO-GB001627.
XX 04-JUN-1997; 97GB-00011579.
XX 20-JUN-1997; 97GB-00013150.
XX 04-JUL-1997; 97GB-00014230.
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
XX WPI; 1999-059910/05.
XX P-PSDB; AAW86004.
XX New vector encoding a tumour interacting protein for treating cancer -
XX contains a desired nucleotide sequence and/or protein which recognises
XX tumours, and is used as a gene delivery system to treat cancer.
XX Example 5; Fig 2; 82pp; English.
XX This DNA sequence encodes B7-1.5T4.1 (see AAW86004), a fusion protein
XX comprising the extracellular domain (amino acids 1-215) of human co-
XX stimulatory molecule B7-1 joined via a flexible peptide linker to an scFv
XX (see AAW86002) derived from murine 5T4 monoclonal antibody. The cDNA can
XX be inserted into vector pCI to allow expression of the fusion protein in
XX mammalian cells. The trophoblast cell surface antigen defined by 5T4 is
XX expressed at high levels on the cells of a wide variety of human tumours.
XX The invention relates to a vector comprising a nucleotide sequence coding
XX for a tumour interacting protein (TIP) and optionally a nucleotide
XX sequence of interest (NOI) which encodes a protein of interest (POI), the
XX vector being capable of delivering the NOI and/or POI to the tumour
XX recognised by the TIP. Delivery can be in vivo or ex vivo. The vector is
XX used to treat cancer, and may also used as a gene delivery system for
XX introducing at least 1 gene encoding a TIP (preferably a tumour binding
XX protein) into a haematopoietic cell lineage. B7-1 is expected to bind
XX specifically to CD28 and CTLA-4 present on human T-cells
XX SQ Sequence 1467 BP; 394 A; 349 C; 352 G; 372 T; 0 U; 0 Other;
Query Match 92.6%; Score 675; DB 2; Length 1467;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 725; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAGGTCACAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 60
Db 739 GAGGTCACAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 798
QY 61 TCCTGCAAGGCTTCGGTTACTCATTCTACTGCTACTACATGCACTGGGTGAAGCAGAGC 120
Db 799 TCCTGCAAGGCTTCGGTTACTCATTCTACTGCTACTACATGCACTGGGTGAAGCAGAGC 858
QY 121 CATGAAAGAGCTTCAGTGAAGTGGAGTGAATTAATCTTAACATGGTGTACTCTCTAC 180
Db 859 CATGAAAGAGCTTCAGTGAAGTGGAGTGAATTAATCTTAACATGGTGTACTCTCTAC 918
QY 181 AACCGAAATTCAGGACCAAGGCCATATTAATCTGTAGACCAAGTCAATCCACCAAGCCTAC 240
Db 919 AACCGAAATTCAGGACCAAGGCCATATTAATCTGTAGACCAAGTCAATCCACCAAGCCTAC 978
QY 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGCTCTATTACTGTGCAAGATCTACT 300
Db 979 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGCTCTATTACTGTGCAAGATCTACT 1038
QY 301 ATGATTACGAATCTGTTATGGACTTACTGGGCTCAAGTAACTCAGTCAACCGTCTCTCA 360
Db 1039 ATGATTACGAATCTGTTATGGACTTACTGGGCTCAAGTAACTCAGTCAACCGTCTCTCA 1098

QY 361 CGTGTGTGGAGCGGTGGTGGCGGCACTGGCGGCGCGGATCTAGTATTGTATGACC 420
Db 1099 GGTGGTGGTGGAGCGGTGGTGGCGGCACTGGCGGCGCGGATCTAGTATTGTATGACC 1158
QY 421 CAGACTCCACATTCTCTCTTTTTCAGCAGGAGACAGGGTTACCATAACTGCAAGGCC 480
Db 1159 CAGACTCCACATTCTCTCTTTTTCAGCAGGAGACAGGGTTACCATAACTGCAAGGCC 1218
QY 481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAGCCAGGGCAGTCTCTTACA 540
Db 1219 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAGCCAGGGCAGTCTCTTACA 1278
QY 541 CTGCTCATATCTTATACATCCAGTCGCTACCGCTGGAGTCCCTGATCGTTCATTGGCAGT 600
Db 1279 CTGCTCATATCTTATACATCCAGTCGCTACCGCTGGAGTCCCTGATCGTTCATTGGCAGT 1338
QY 601 GGATATGGGACGGATTTTCACATTCACCATCAGCACTTTGCAAGGCTGAAGACCTGGCAGTT 660
Db 1339 GGATATGGGACGGATTTTCACATTCACCATCAGCACTTTGCAAGGCTGAAGACCTGGCAGTT 1398
QY 661 TATTTCTGTACGACAGATTATTAATTTCTCCGAGCTTCGGTGGAGGCACCAAGCTGGAA 720
Db 1399 TATTTCTGTACGACAGATTATTAATTTCTCCGAGCTTCGGTGGAGGCACCAAGCTGGAA 1458
QY 721 ATCAAA 726
Db 1459 ATCAAA 1464
RESULT 7
AAF89730
ID AAF89730 standard; DNA; 1467 BP.
XX
AC AAF89730;
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of a B7-1.5T4.1 fusion protein.
XX
KW Single chain antibody; scFv; inflammatory disease; arthritis; cancer;
KW hypersensitivity; autoimmune disease; central nervous system disorder;
KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW Helicobacter-related disease; immune disorder; ss.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1467
FT /*tag= a
XX
XX WO200136486-A2.
XX 25-MAY-2001.
XX
XX 13-NOV-2000; 2000WO-GB004317.
XX
XX 18-NOV-1999; 99WO-GB003859.
XX 15-FEB-2000; 2000GB-00003527.
XX 02-MAR-2000; 2000GB-00005071.
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
XX Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
XX Myers KA;
XX WPI; 2001-343805/36.
XX P-PSDB; AAB83836.
XX
XX Use of single chain antibody capable of recognizing a disease associated
XX molecule for manufacturing a medicament for preventing and/or treating a
XX

QY 61 TCCTGCAAGGCTTCTGTTACTCATTCACCTGGCTACTACATGACCTGGGTGAAGCAGAC 120
 Db 847 TCCTGCAAGGCTTCTGTTACTCATTCACCTGGCTACTACATGACCTGGGTGAAGCAGAC 906
 QY 121 CATGGAAGAGCCTTGAGTGGATTGACAGTATTAATCCTAAAGTGTACTCTCTAC 180
 Db 907 CATGGAAGAGCCTTGAGTGGATTGACAGTATTAATCCTAAAGTGTACTCTCTAC 966
 QY 181 AACGAGAAATTCAGAGCAGGCCATATTAACCTGTAGCAAGTCATCCACCAAGCCTAC 240
 Db 967 AACGAGAAATTCAGAGCAGGCCATATTAACCTGTAGCAAGTCATCCACCAAGCCTAC 1026
 QY 241 ATGGAGCTCCGACGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
 Db 1027 ATGGAGCTCCGACGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086
 QY 301 ATGATTACGAACATATGTTATGAGTACTCTGGGTCAAGTAACTCAGTCAACCTCTCTCA 360
 Db 1087 ATGATTACGAACATATGTTATGAGTACTCTGGGTCAAGTAACTCAGTCAACCTCTCTCA 1146
 QY 361 GGTGGTGGTGGAGCGGTGGTGGCGCACTGGCGGGCGGATCTAGTATTCTGTGATGACC 420
 Db 1147 GGTGGTGGTGGAGCGGTGGTGGCGCACTGGCGGGCGGATCTAGTATTCTGTGATGACC 1206
 QY 421 CAGACTCCACATCTCTGCTTGTTCAGCAGGAGCAGGGTTACCATACCTGCAAGGCC 480
 Db 1207 CAGACTCCACATCTCTGCTTGTTCAGCAGGAGCAGGGTTACCATACCTGCAAGGCC 1266
 QY 481 AGTCAGAGTGTGATGATGATGTTGGTACCAACAGAACCCAGGGCAGTCTCTTACA 540
 Db 1267 AGTCAGAGTGTGATGATGATGTTGGTACCAACAGAACCCAGGGCAGTCTCTTACA 1326
 QY 541 CTGCTCATATCTATACATCCAGTCTGCTACGCTGGAGTCCCTGATCGCTTCAATTCGCACT 600
 Db 1327 CTGCTCATATCTATACATCCAGTCTGCTACGCTGGAGTCCCTGATCGCTTCAATTCGCACT 1386
 QY 601 GGATATGGAGCGGATTTCACTTTCCACATFAGCACTTTGCAAGGCTGAAGACCTGCGAGTT 660
 Db 1387 GGATATGGAGCGGATTTCACTTTCCACATFAGCACTTTGCAAGGCTGAAGACCTGCGAGTT 1446
 QY 661 TATTTCTGTCCAGCAAGATTAATTTCTCTCCGAGTTCGTTGGTGGAGGCCACCAAGCTGAA 720
 Db 1447 TATTTCTGTCCAGCAAGATTAATTTCTCTCCGAGTTCGTTGGTGGAGGCCACCAAGCTGAA 1506
 QY 721 ATCAAACGG 729
 Db 1507 ATCAAACGG 1515

RESULT 9

AAF89732

ID AAF89732 standard; DNA; 1518 BP.

AC XX

AC AAF89732;

XX XX

DT 23-JUL-2001 (first entry)

XX XX

DE Nucleotide sequence of a B7 link ScFv sequence.

XX XX

KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
 KW hypersensitivity; autoimmune disease; central nervous system disorder;
 KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
 KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
 KW Helicobacter-related disease; immune disorder; ss.

OS Synthetic.

OS Homo sapiens.

XX XX

FN WO200136486-A2.

XX XX

PD 25-MAY-2001.

XX XX

13-NOV-2000; 2000WO-GB004317.
 18-NOV-1999; 99WO-GB003859.
 15-FEB-2000; 2000GB-00003527.
 02-MAR-2000; 2000GB-00005071.
 (OXFO-) OXFORD BIOMEDICA UK LTD.
 Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
 Myers KA;
 WPI; 2001-343805/36.
 Use of single chain antibody capable of recognizing a disease associated
 molecule for manufacturing a medicament for preventing and/or treating a
 disease condition associated with disease associated molecule.
 Example 8; Fig 5; 118pp; English.

The specification describes the use of a single chain antibody (ScFv),
 which is capable of recognizing a disease associated molecule in the
 manufacture of a medicament for the prevention and treatment of a disease
 condition. The ScFv antibody is useful in the manufacture of a
 medicament, for affecting a disease in vivo, for preparing a
 pharmaceutical composition, for in vivo imaging and/or for adjuvant
 treatment of a disease. The ScFv antibody is also useful for treating
 inflammatory diseases including arthritis, hypersensitivity, autoimmune
 diseases, cancers, central nervous system disorders including Parkinson's
 disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
 diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
 related diseases, and other immune disorders. The present sequence
 encodes a B7 link ScFv sequence. A human B7 sequence is linked to a ScFv
 of the invention

Sequence 1518 BP; 398 A; 364 C; 371 G; 385 T; 0 U; 0 Other;

Query Match 79.0%; Score 576; DB 4; Length 1518;

Best Local Similarity 99.6%; Pred. No. 9.6e-270;

Matches 726; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGTCCAGCTTTCAGCAGTCTGGACCTGACCTGGTGAAGCTTGGGCTTCAGTGAAGATA 60
 Db 787 GAGTCCAGCTTTCAGCAGTCTGGACCTGACCTGGTGAAGCTTGGGCTTCAGTGAAGATA 846
 QY 61 TCCTGCAAGGCTTCTGTTACTCATTCACCTGGCTACTACATGCACTGGGTGAAGCAGAC 120
 Db 847 TCCTGCAAGGCTTCTGTTACTCATTCACCTGGCTACTACATGCACTGGGTGAAGCAGAC 906
 QY 121 CATGGAAGAGCCTTGAGTGGATTGAGTGGACGTATTAATCCTAAAGTGTGTTACTCTCTAC 180
 Db 907 CATGGAAGAGCCTTGAGTGGATTGAGTGGACGTATTAATCCTAAAGTGTGTTACTCTCTAC 966
 QY 181 AACGAGAAATTCAGAGCAGGCCATATTAACCTGTAGCAAGTCATCCACCAAGCCTAC 240
 Db 967 AACGAGAAATTCAGAGCAGGCCATATTAACCTGTAGCAAGTCATCCACCAAGCCTAC 1026
 QY 241 ATGGAGCTCCGACGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
 Db 1027 ATGGAGCTCCGACGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086
 QY 301 ATGATTACGAACATATGTTATGAGTACTCTGGGTCAAGTAACTCAGTCAACCTCTCTCA 360
 Db 1087 ATGATTACGAACATATGTTATGAGTACTCTGGGTCAAGTAACTCAGTCAACCTCTCTCA 1146
 QY 361 GGTGGTGGTGGAGCGGTGGTGGCGCACTGGCGGGCGGATCTAGTATTCTGTGATGACC 420
 Db 1147 GGTGGTGGTGGAGCGGTGGTGGCGCACTGGCGGGCGGATCTAGTATTCTGTGATGACC 1206
 QY 421 CAGACTCCACATTTCTCTGCTTGTTCAGCAGGAGCAGGGTTACCATACCTGCAAGGCC 480
 Db 1207 CAGACTCCACATTTCTCTGCTTGTTCAGCAGGAGCAGGGTTACCATACCTGCAAGGCC 1266
 QY 481 AGTCAGAGTGTGATGATGATGTTGGTACCAACAGAACCCAGGGCAGTCTCTTACA 540

Db 1267 AGTCAGAGTGTGAGTAATGATAGCTTGGTACCAACAGAGCCAGGGCAGTCTCTTACA 1326
Qy 541 CTGCTCATATCCTATACATCCAGTGGTACGCTGGAGTCCCTGATCGCTTCAATTGGCAGT 600
Db 1327 CTGCTCATATCCTATACATCCAGTGGTACGCTGGAGTCCCTGATCGCTTCAATTGGCAGT 1386
Qy 601 GGATATGGACCGATTTCACTTTTCCACCATCAGCATCTTTGCGAGCTTGAAGACCTGGCAGTT 660
Db 1387 GGATATGGACCGATTTCACTTTTCCACCATCAGCATCTTTGCGAGCTTGAAGACCTGGCAGTT 1446
Qy 661 TATTTCTGTCCACAGATTAATTTCTCTCCGAGCTTGGTGGAGGACCAAGCTGGAA 720
Db 1447 TATTTCTGTCCACAGATTAATTTCTCTCCGAGCTTGGTGGAGGACCAAGCTGGAA 1506
Qy 721 ATCAAACGG 729
Db 1507 ATCAAACGG 1515

RESULT 10
AAFP89733
ID AAF89733 standard; DNA; 1796 BP.
AC AAF89733;
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of an Ig-574 fusion protein.
XX
KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW hypersensitivity; autoimmune disease; central nervous system disorder;
KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW Helicobacter-related disease; immune disorder; ss.
XX
OS Synthetic.
OS Mus sp.
XX
FH Key
FT CDS
FT Location/Qualifiers
FT 12..1790
FT /*tag= a
FT /transl_except= (1518..1520, aa: Met)
XX
PN WO200136486-A2.
XX
PD 25-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-GB004317.
XX
PR 18-NOV-1999; 99WO-GB003859.
PR 15-FEB-2000; 2000GB-00003527.
PR 02-MAR-2000; 2000GB-00005071.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingman A, Kingman SM, Bebbington CR, Carroll MW, Ellard FW;
PI Myers KA;
XX
DR WPI; 2001-343805/36.
DR P-PSDB; AAB83838.
XX

Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
XX
PS Claim 9; Fig 6; 118pp; English.
XX
CC The specification describes the use of a single chain antibody (ScFv),
CC which is capable of recognizing a disease associated molecule in the
CC manufacture of a medicament for the prevention and treatment of a disease
CC condition. The ScFv antibody is useful in the manufacture of a
CC medicament, for affecting a disease in vivo, for preparing a

CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC treatment of a disease. The ScFv antibody is also useful for treating
CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC disease, cancers, central nervous system disorders including Parkinson's
CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC disease, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC related diseases, and other immune disorders. The present sequence
CC encodes an Ig-574 fusion protein
XX
SQ Sequence 1796 BP; 429 A; 539 C; 466 G; 362 T; 0 U; 0 Other;

Query Match 75.6%; Score 551; DB 4; Length 1796;
Best Local Similarity 99.6%; Pred. No. 1.4e-257;
Matches 701; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 13 CAGCAGTCTGGACCTGACCTGGTGAAGCTTGGGGCTTCAGTGAAGATATCTTCGAAGGCT 72
Db 81 CAGCAGTCTGGACCTGACCTGGTGAAGCTTGGGGCTTCAGTGAAGATATCTTCGAAGGCT 140
Qy 73 TCTGTTACTCATTTCACTGGCTACTACATGCACTGGGTGAAGCAGCAGCCATGGAAGAGC 132
Db 141 TCTGTTACTCATTTCACTGGCTACTACATGCACTGGGTGAAGCAGCAGCCATGGAAGAGC 200
Qy 133 CTTCGAGTGGATTGGACGCTATTAACTCTTAACAATGGTGTACTCTCTACAACAGAAATTC 192
Db 201 CTTCGAGTGGATTGGACGCTATTAACTCTTAACAATGGTGTACTCTCTACAACAGAAATTC 260
Qy 193 AAGACAAGGCGCATATTAACTGTAGACAAGTCAATCCACACAGCCCTACATGAGGCTCCG 252
Db 261 AAGACAAGGCGCATATTAACTGTAGACAAGTCAATCCACACAGCCCTACATGAGGCTCCG 320
Qy 253 AGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATGAGAAC 312
Db 321 AGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATGAGAAC 380
Qy 313 TATGTTATGGACTACTGGGTCAAGTCACTCAGTCAGGCTCTCTCAGGTGGTGGG 372
Db 381 TATGTTATGGACTACTGGGTCAAGTCACTCAGTCAGGCTCTCTCAGGTGGTGGG 440
Qy 373 AGCGTGGTGGCGGACCTGGCGGCGGATCTAGTATTGTGATGATGATGATGATGATGATG 432
Db 441 AGCGTGGTGGCGGACCTGGCGGCGGATCTAGTATTGTGATGATGATGATGATGATGATG 500
Qy 433 TTCCTGCTTTTTCAGCAGGAGACAGGGTTACCAATAACCTGCAAGGCCAGTCAAGTGTG 492
Db 501 TTCCTGCTTTTTCAGCAGGAGACAGGGTTACCAATAACCTGCAAGGCCAGTCAAGTGTG 560
Qy 493 AGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 552
Db 561 AGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 620
Qy 553 TATACATCCAGTCCGCTACGCTGGAGTCCCTGATCCCTTCATTGGCAGTGGATATGGAGC 612
Db 621 TATACATCCAGTCCGCTACGCTGGAGTCCCTGATCCCTTCATTGGCAGTGGATATGGAGC 680
Qy 613 GATTTCACTTTTCCACCATCAGCATTTCAGAGCTGAAGACCTGGCAGTTTATTTCTGTAG 672
Db 681 GATTTCACTTTTCCACCATCAGCATTTCAGAGCTGAAGACCTGGCAGTTTATTTCTGTAG 740
Qy 673 CAAGATTATATTTCTCTCCGACGTTTCGGTGGAGGCCACCAAGCT 716
Db 741 CAAGATTATATTTCTCTCCGACGTTTCGGTGGAGGCCACCAAGCT 784

RESULT 11
AAV80295
ID AAV80295 standard; cDNA; 2090 BP.
XX
AC AAV80295;
XX
DT 15-MAR-1999 (first entry)
XX
DE ScFv-IgE1 fusion construct for use in cancer gene therapy.

XX Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW monoclonal antibody; single chain antibody; scFv; mouse; human; IgE1; ss.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
XX WO985607-A2.
XX
XX 10-DEC-1998.
XX
XX 04-JUN-1998; 98WO-GB001627.
XX
XX 04-JUN-1997; 97GB-00011579.
PR 20-JUN-1997; 97GB-00013150.
PR 04-JUL-1997; 97GB-00014230.
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
XX Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
PI
DR WPI; 1999-059910/05.
XX
XX New vector encoding a tumour interacting protein for treating cancer -
PT contains a desired nucleotide sequence and/or protein which recognises
PT tumours, and is used as a gene delivery system to treat cancer.
XX
XX Example 13; Page 64; 82pp; English.
XX
XX This DNA sequence encodes a fusion protein comprising the human IgE1
CC heavy constant region joined via a flexible peptide linker to an scFv
CC (see AAW86002) derived from murine 5T4 monoclonal antibody. The fusion
CC construct can be incorporated into a recombinant viral vector for use in
CC gene therapy of cancer. The trophoblast cell surface antigen defined by
CC 5T4 is expressed at high levels on the cells of a wide variety of human
CC tumours. Binding of IgE to tumour cells should promote a strong histamine
CC and hence inflammatory response and destruction of tumour cells. The
CC invention relates to a vector comprising a nucleotide sequence coding for
CC a tumour interacting protein (TIP) and optionally a nucleotide sequence
CC of interest (NOI) which encodes a protein of interest (POI), the vector
CC being capable of delivering the NOI and/or POI to the tumour recognised
CC by the TIP. Delivery can be in vivo or ex vivo
XX
SQ Sequence 2090 BP; 461 A; 653 C; 565 G; 411 T; 0 U; 0 Other;

Query Match 75.6%; Score 551; DB 2; Length 2090;
Best Local Similarity 99.6%; Pred. No. 1.4e-257;
Matches 701; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 CAGCAGTCTGGACCTGACCTGGTGAAGCTGGGGCTTCAGTGAAGATATCTGCAAGCT 72
Db 81 CAGCAGTCTGGACCTGACCTGGTGAAGCTGGGGCTTCAGTGAAGATATCTGCAAGCT 140
QY 73 TCTGGTTACTCATTCACCTGGCTTACTACATGCACTGGGTGAAGCAGCAGCATGGAAGAGC 132
Db 141 TCTGGTTACTCATTCACCTGGCTTACTACATGCACTGGGTGAAGCAGCAGCATGGAAGAGC 200
QY 133 CTTGAGTGGAATTGGACGTATTAAATCCTAACATGGTGTACTCTCTACAAACAGAAATTC 192
Db 201 CTTGAGTGGAATTGGACGTATTAAATCCTAACATGGTGTACTCTCTACAAACAGAAATTC 260
QY 193 AAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACAGCTACATGAGCTCCG 252
Db 261 AAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACAGCTACATGAGCTCCG 320
QY 253 AGCCTGACATCTGAGGACTCTCGGCTTATTACTGTGCAAGATCTACTGATTACGAAC 312
Db 321 AGCCTGACATCTGAGGACTCTCGGCTTATTACTGTGCAAGATCTACTGATTACGAAC 380
QY 313 TATGTTATGGACTACTGGGTCGAAGTAACTCAGTCACCGTCTCTCAGGTGGTGGG 372

Db 381 TATGTTATGGACTACTGGGTCGAAGTAACTCAGTCACCGTCTCTTCAAGTGGTGGTGGG 440
QY 373 AGCGTGGTGGCGGCACTGGCGGGCGGAGTCTAGTATTTGTGATGA CCCAGACTCCCA 432
Db 441 AGCGTGGTGGCGGCACTGGCGGGCGGAGTCTAGTATTTGTGATGA CCCAGACTCCCA 500
QY 433 TTCCTGCTTTTTCAGCAGGAGACAGGGTTACCAATACCTGCAAGGCCAGTCAGAGTGTG 492
Db 501 TTCCTGCTTTTTCAGCAGGAGACAGGGTTACCAATACCTGCAAGGCCAGTCAGAGTGTG 560
QY 493 AGTAATGATGTAGDTTGGTACCAACAGAGCCAGGCGAGTCTCCTACACTGCTCATATCC 552
Db 561 AGTAATGATGTAGCTTGGTACCAACAGAGCCAGGCGAGTCTCCTACACTGCTCATATCC 620
QY 553 TATACATCCAGTCGCTAGCTGGAGTCCCTGATCGCTTCATTTGGCAGTGGATATGGAGC 612
Db 621 TATACATCCAGTCGCTAGCTGGAGTCCCTGATCGCTTCATTTGGCAGTGGATATGGAGC 680
QY 613 GATTTCACTTTTCCACATCAGCACCTTTCGAGGCTGAAGACCTGGCAGTTTATTTCTGTGAG 672
Db 691 GATTTCACTTTTCCACATCAGCACCTTTCGAGGCTGAAGACCTGGCAGTTTATTTCTGTGAG 740
QY 673 CAAGATTATATTTCTCTCCGACGTTGGTGGAGGCCACCAAGCT 716
Db 741 CAAGATTATATTTCTCTCCGACGTTGGTGGAGGCCACCAAGCT 784
RESULT 12
AAF89734
ID AAF89734 standard; DNA; 2090 BP.
XX
AC AAF89734;
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of a SvFv-IgE protein.
XX
KW Single chain antibody; scFv; inflammatory disease; arthritis; cancer;
KW hypersensitivity; autoimmune disease; central nervous system disorder;
KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW Helicobacter-related disease; immune disorder; ss.
XX
OS Synthetic.
XX
XX WO200136486-A2.
XX
PD 25-MAY-2001.
XX
XX 13-NOV-2000; 2000WO-GB004317.
XX
PR 18-NOV-1999; 99WO-GB0003859.
PR 15-FEB-2000; 2000GB-00003527.
PR 02-MAR-2000; 2000GB-00005071.
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
XX Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
PI Myers KA;
XX
XX WPI; 2001-343805/36.
XX
PT Use of single chain antibody capable of recognizing a disease associated
PT molecule for manufacturing a medicament for preventing and/or treating a
PT disease condition associated with disease associated molecule.
XX
XX Example 11; Fig 7; 118pp; English.
XX
XX The specification describes the use of a single chain antibody (scFv),
CC which is capable of recognizing a disease associated molecule in the
CC manufacture of a medicament for the prevention and treatment of a disease
CC condition. The scFv antibody is useful in the manufacture of a
CC medicament, for affecting a disease in vivo, for preparing a

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CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC treatment of a disease. The ScFv antibody is also useful for treating
CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC diseases, cancers, central nervous system disorders including Parkinson's
CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC related diseases, and other immune disorders. The present sequence
CC encodes a ScFv of the invention linked to an Igb sequence
XX
SQ Sequence 2090 BP; 461 A; 654 C; 564 G; 411 T; 0 U; 0 Other;
Query Match 75.6%; Score 551; DB 4; Length 2090;
Best Local Similarity 99.6%; Pred. No. 1.4e-257;
Matches 701; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 13 CAGCAGTCTGGACCTGACCTGGTGAAGCTGGGGCTTCAAGTGAAGATATCTTCAAGGCT 72
DB 81 CAGCAGTCTGGACCTGACCTGGTGAAGCTGGGGCTTCAAGTGAAGATATCTTCAAGGCT 140
QY 73 TCTGGTTACTCATTTCACTGGCTACTACATGCACTGGGTGAAGCAGCAGCCATGGAAGAGC 132
DB 141 TCTGGTTACTCATTTCACTGGCTACTACATGCACTGGGTGAAGCAGCAGCCATGGAAGAGC 200
QY 133 CTTGAGTGGATTGGAGCTATTATCTTAACAATGGTTACTCTCTACAAACAGAAATTC 192
DB 201 CTTGAGTGGATTGGAGCTATTATCTTAACAATGGTTACTCTCTACAAACAGAAATTC 260
QY 193 AAGGACAAGGCCATATTAACTGTAGACAAGTCAATCCACCACAGCCTTACATGAGCTCCGC 252
DB 261 AAGGACAAGGCCATATTAACTGTAGACAAGTCAATCCACCACAGCCTTACATGAGCTCCGC 320
QY 253 AGCCTGACATCTGAGGACTCTCGGCTTATTACTGTGCAAGATCTACTATGATTACGAAAC 312
DB 321 AGCCTGACATCTGAGGACTCTCGGCTTATTACTGTGCAAGATCTACTATGATTACGAAAC 380
QY 313 TATGTTATGCACTACTGGGCTCAAGTAACTCAGTCACCGTCTCTCAGTGGTGGTGG 372
DB 381 TATGTTATGCACTACTGGGCTCAAGTAACTCAGTCACCGTCTCTCAGTGGTGGTGG 440
QY 373 AGCGTGGTGGCGGCACTGGCGGCGCGGATCTAGTATTTGTATGATCAACCCAGACTCCCA 432
DB 441 AGCGTGGTGGCGGCACTGGCGGCGCGGATCTAGTATTTGTATGATCAACCCAGACTCCCA 500
QY 433 TTCTGCTGTTTTCACAGAGAGACAGGGTTACATAACCTGCAAGCCAGTCCAGAGTGTG 492
DB 501 TTCTGCTGTTTTCACAGAGAGACAGGGTTACATAACCTGCAAGCCAGTCCAGAGTGTG 560
QY 493 AGTAATGATGTAGTTGGTTACCAACAGAGCCAGGCGAGTCTCTACACTGCTCATATCC 552
DB 561 AGTAATGATGTAGTTGGTTACCAACAGAGCCAGGCGAGTCTCTACACTGCTCATATCC 620
QY 553 TATACATCCAGTCCGCTACGCTGAGTCCCTGATCGCTTCATTGGCAGTGGATATGGAGC 612
DB 621 TATACATCCAGTCCGCTACGCTGAGTCCCTGATCGCTTCATTGGCAGTGGATATGGAGC 680
QY 613 GATTTCACTTTCCATCAGCAGCTTTGCAAGGCTGAAGACCTGGCAGTTTATTCTGTGAG 672
DB 681 GATTTCACTTTCCATCAGCAGCTTTGCAAGGCTGAAGACCTGGCAGTTTATTCTGTGAG 740
QY 673 CAAGATTATTAATTCCTCCGACGTTTCGTTGAGGACCAAGCT 716
DB 741 CAAGATTATTAATTCCTCCGACGTTTCGTTGAGGACCAAGCT 784
RESULT 13
AAQ73679
ID AAQ73679 standard; DNA; 729 BP.
XX
AC AAQ73679;
XX
DT 25-MAR-2003 (revised)
DT 09-MAY-1995 (first entry)
XX
```

```
DE Fv(GP-4) immunosuppressive.
XX
KW MAb; monoclonal antibody; hybridoma; interleukin-2; IL-2; Fv;
KW antibody variable region; GP-4; Fv(GP-4); immunosuppressive; ss.
XX
OS Mus sp.
XX
PN EP621338-A2.
XX
PD 26-OCT-1994.
XX
XX 21-APR-1994; 94EP-00106257.
XX
XX 21-APR-1993; 93JP-00094491.
PR 07-MAR-1994; 94JP-00036065.
XX
XX (AJIN ) AJINOMOTO KK.
XX
PI Shimamura T, Hamura J, Nakazawa H, Kanayama Y, Sugamura K;
PI Takeshita T;
XX
XX WPI; 1994-325948/41.
DR P-PSDB; AAR60781.
XX
XX Immunosuppressant polypeptide - has ability to block interleukin-2
PT response.
XX
XX Claim 18; Page 29; 37pp; English.
XX
CC MAb capable of binding to the gamma chain of the IL-2 receptor, and thus
CC of blocking the IL-2 response, is produced by mouse hybridoma line GP-4
CC (FERM BP-4640). DNA encoding the variable region of this MAb was
CC expressed in E. coli, yielding Fv(GP-4) with immunosuppressive activity.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 729 BP; 199 A; 169 C; 182 G; 179 T; 0 U; 0 Other;
Query Match 11.8%; Score 86; DB 2; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.3e-31;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTCGAAGGCTTCTGGTTACTCATTCCT 90
DB 397 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTCGAAGGCTTCTGGTTACTCATTCCT 456
QY 91 GGCTACTACATGCATCGGTGAAGCA 116
DB 457 GGCTACTACATGCATCGGTGAAGCA 482
RESULT 14
ADM72026
ID ADM72026 standard; DNA; 1413 BP.
XX
AC ADM72026;
XX
XX 03-JUN-2004 (first entry)
XX
DE Chimeric mouse-human antibody M1E07 heavy chain encoding DNA.
XX
KW GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer;
KW cytotstatic; gene; ds; M1E07.
XX
XX Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
XX Key 1..1413 location/Qualifiers
XX CDS /*tag= a
XX FT /product= "M1E07 heavy chain"
XX
PN WO2004022739-A1.
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XX PD 18-MAR-2004.
XX XX
XX PF 04-SEP-2003; 2003WO-JF011318.
XX PR 04-SEP-2002; 2002WO-JF008999.
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX PI Aburatani H, Midorikawa Y, Nakano K, Ohizumi I, Ito Y, Tokita S;
XX DR WPI; 2004-269573/25.
XX DR P-PSDB; ADM72027.
XX PT Antibody against the N terminus of glypican 3 (GPC3) causes cell
XX PT disruption and is useful as an anticancer agent.
XX PS Example 4; SEQ ID NO 11; 122pp; Japanese.
XX CC The invention relates to an antibody against the N terminus of glypican 3
XX CC (GPC3). The antibody can be used for causing cell disruption and can be
XX CC used as an anti-cancer agent. The present sequence represents a chimeric
XX CC mouse-human antibody M1E07 heavy chain encoding DNA.
XX SQ Sequence 1413 BP; 340 A; 436 C; 372 G; 265 T; 0 U; 0 Other;

Query Match 11.8%; Score 86; DB 12; Length 1413;
Best Local Similarity 100.0%; Pred. No. 2.2e-31;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTGCAAGGCTTCGTGTTACTCAATTCAC 90
DB 88 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTGCAAGGCTTCGTGTTACTCAATTCAC 147

QY 91 GGCTACTACATGCATCGGCTGAAGCA 116
DB 148 GGCTACTACATGCATCGGCTGAAGCA 173

RESULT 15
AAT43737
ID AAT43737 standard; cDNA; 334 BP.
XX AC AAT43737;
XX DT 27-AUG-2003 (revised)
XX DT 12-AUG-1997 (first entry)
XX DE Anti-DNA antibody 7b3 heavy chain variable region cDNA.
XX KW Heavy chain; variable region; anti-DNA; monoclonal; antibody; MAb 7b3;
XX KW hairpin; diagnosis; inflammatory glomerulonephritis;
XX KW systemic lupus erythematosus; screening; treatment; prevention; SLE;
XX KW disease; ss.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT CDS 2..334
XX FT /tag= a
XX FT /note= "no STOP codon given"
XX PN WO9636361-A1.
XX PD 21-NOV-1996.
XX PF 16-MAY-1996; 96WO-US007113.
XX PR 18-MAY-1995; 95US-00443540.
XX PA (UNMI ) UNIV MICHIGAN.
XX PI Glick GD, Swanson PC;

```

```

XX DR WPI; 1997-011854/01.
XX PT Anti-DNA antibody which specifically binds DNA hairpin - useful to
XX PT develop prods. for diagnosis and treatment of disorders, e.g.
XX PT glomerulonephritis or systemic lupus erythematosus.
XX PS Example; Fig 7; 102pp; English.
XX CC The present sequence encodes the heavy chain variable region of the anti-
XX CC DNA monoclonal antibody (MAb) 7b3, which has a high affinity for single
XX CC stranded DNA, low or no affinity for double stranded DNA and specifically
XX CC binds a DNA hairpin. The MAb can be used to diagnose disorders associated
XX CC with the pathological complexation of DNA, e.g. inflammatory
XX CC glomerulonephritis and systemic lupus erythematosus. It can also be used
XX CC to generate reagents to screen for pharmaceutical agents, and treat
XX CC and/or prevent an above disorder. Calf thymus DNA was used to immunise a
XX CC MRL-lpr mouse, spleen cells from which were then fused with Sp2/0 myeloma
XX CC cells to give hybridomas producing the anti-DNA MAb. 7b3 was found to
XX CC react strongly with poly(dT), poly(GG) and poly(GI), moderately with
XX CC single stranded DNA and weakly with poly(G). (Updated on 27-AUG-2003 to
XX CC correct OS field.)
XX SQ Sequence 334 BP; 93 A; 79 C; 83 G; 79 T; 0 U; 0 Other;

Query Match 9.1%; Score 66; DB 2; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTGCAAGGCTTCGTGTTACTCAATTCAC 90
DB 8 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTGCAAGGCTTCGTGTTACTCAATTCAC 67

QY 91 GGCTAC 96
DB 68 GGCTAC 73

Search completed: March 15, 2005, 21:19:17
Job time : 591 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 20:44:30 ; Search time 236 Seconds
(without alignments)
5054.431 Million cell updates/sec

Title: US-10-016-686-5
Perfect score: 729
Sequence: 1 gaggtccagcttcagcagtc.....ccaagctggaatcaaacgg 729

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818139359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1 | 86 | 11.8 | 729 | 1 US-08-230-843-3 | Sequence 3, Appli |
| 2 | 86 | 11.8 | 729 | 2 US-08-636-936-3 | Sequence 3, Appli |
| 3 | 66 | 9.1 | 334 | 3 US-08-881-037-11 | Sequence 11, Appli |
| 4 | 63 | 8.6 | 906 | 2 US-08-656-906-24 | Sequence 24, Appli |
| 5 | 63 | 8.6 | 906 | 3 US-09-217-847-24 | Sequence 24, Appli |
| 6 | 62 | 8.5 | 318 | 1 US-08-463-128-2 | Sequence 2, Appli |
| 7 | 62 | 8.5 | 318 | 1 US-08-463-298-2 | Sequence 2, Appli |
| 8 | 62 | 8.5 | 318 | 2 US-08-436-339A-2 | Sequence 2, Appli |
| 9 | 62 | 8.5 | 318 | 2 US-08-822-830B-3 | Sequence 3, Appli |
| 10 | 62 | 8.5 | 318 | 2 US-08-950-660-3 | Sequence 3, Appli |
| 11 | 62 | 8.5 | 318 | 4 US-09-157-452B-3 | Sequence 3, Appli |
| 12 | 62 | 8.5 | 318 | 4 US-08-454-899G-9 | Sequence 9, Appli |
| 13 | 62 | 8.5 | 318 | 5 PCT-US93-00030-3 | Sequence 3, Appli |
| 14 | 62 | 8.5 | 318 | 5 PCT-US93-00924-3 | Sequence 3, Appli |
| 15 | 62 | 8.5 | 318 | 5 PCT-US94-10395-2 | Sequence 2, Appli |
| 16 | 59 | 8.1 | 714 | 3 US-09-142-974B-2 | Sequence 2, Appli |
| 17 | 59 | 8.1 | 1173 | 3 US-09-143-974B-4 | Sequence 4, Appli |
| 18 | 56 | 7.7 | 405 | 1 US-08-137-117D-26 | Sequence 26, Appli |
| 19 | 56 | 7.7 | 405 | 1 US-08-436-717-26 | Sequence 26, Appli |
| 20 | 56 | 7.7 | 1425 | 4 US-09-592-998C-6 | Sequence 6, Appli |
| 21 | 52 | 7.1 | 344 | 2 US-08-888-366-7 | Sequence 7, Appli |
| 22 | 52 | 7.1 | 372 | 3 US-09-257-069-1 | Sequence 1, Appli |
| 23 | 52 | 7.1 | 372 | 4 US-10-007-790-1 | Sequence 1, Appli |
| 24 | 52 | 7.1 | 405 | 1 US-08-398-613A-49 | Sequence 49, Appli |
| 25 | 52 | 7.1 | 405 | 1 US-08-398-612A-49 | Sequence 49, Appli |
| 26 | 52 | 7.1 | 405 | 1 US-08-398-611A-49 | Sequence 49, Appli |
| 27 | 52 | 7.1 | 405 | 1 US-08-396-851A-49 | Sequence 49, Appli |

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|----|----|-----|-----|---------------------|--------------------|
| 28 | 52 | 7.1 | 405 | 2 US-08-491-334A-49 | Sequence 49, Appli |
| 29 | 52 | 7.1 | 405 | 3 US-09-027-449-36 | Sequence 36, Appli |
| 30 | 52 | 7.1 | 405 | 3 US-08-804-444A-36 | Sequence 36, Appli |
| 31 | 52 | 7.1 | 405 | 3 US-09-026-985-36 | Sequence 36, Appli |
| 32 | 52 | 7.1 | 405 | 3 US-09-121-952A-36 | Sequence 36, Appli |
| 33 | 52 | 7.1 | 405 | 3 US-09-234-340A-36 | Sequence 36, Appli |
| 34 | 52 | 7.1 | 738 | 1 US-08-197-834-6 | Sequence 6, Appli |
| 35 | 52 | 7.1 | 762 | 1 US-08-398-613A-57 | Sequence 57, Appli |
| 36 | 52 | 7.1 | 762 | 1 US-08-398-612A-57 | Sequence 57, Appli |
| 37 | 52 | 7.1 | 762 | 1 US-08-398-611A-57 | Sequence 57, Appli |
| 38 | 52 | 7.1 | 762 | 1 US-08-396-851A-57 | Sequence 57, Appli |
| 39 | 52 | 7.1 | 762 | 2 US-08-491-334A-57 | Sequence 57, Appli |
| 40 | 52 | 7.1 | 762 | 3 US-09-027-449-43 | Sequence 43, Appli |
| 41 | 52 | 7.1 | 762 | 3 US-08-804-444A-43 | Sequence 43, Appli |
| 42 | 52 | 7.1 | 762 | 3 US-09-026-985-43 | Sequence 43, Appli |
| 43 | 52 | 7.1 | 762 | 3 US-09-121-952A-43 | Sequence 43, Appli |
| 44 | 52 | 7.1 | 762 | 3 US-09-234-340A-43 | Sequence 43, Appli |
| 45 | 51 | 7.0 | 324 | 4 US-09-486-814A-3 | Sequence 3, Appli |

ALIGNMENTS

RESULT 1
US-08-230-843-3
; Sequence 3, Application US/08230843
; Patent No. 5582826
; GENERAL INFORMATION:
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: HAMURO, JUNJI
; APPLICANT: NAKAZAWA, HARUMI
; APPLICANT: KANAYAMA, YUKA
; APPLICANT: SUGAMURA, KAZUO
; APPLICANT: TAKESHITA, TOSHIKAZU
; TITLE OF INVENTION: IMMUNOSUPPRESSANT
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,843
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 094491/1993
; FILING DATE: 21-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 036065/1994
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5582826man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0674-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 729 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

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; MOLECULE TYPE: Other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..729
US-08-230-843-3
Query Match      11.8%; Score 86; DB 1; Length 729;
Best Local Similarity 100.0%; Pred. No. 1e-33;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTGCAAGGCTTCTGGTTACTCAATCACT 90
Db 397 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTGCAAGGCTTCTGGTTACTCAATCACT 456

QY 91 GGCTACTACATGCACCTGGGTGAAGCA 116
Db 457 GGCTACTACATGCACCTGGGTGAAGCA 482

RESULT 2
US-08-636-936-3
; Sequence 3, Application US/08636936
; Patent No. 5856140
; GENERAL INFORMATION:
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: HAMURO, JUNJI
; APPLICANT: NAKAZAWA, HARUMI
; APPLICANT: KANAYAMA, YUKA
; APPLICANT: SUGAMURA, KAZUO
; APPLICANT: TAKESHITA, TOSHIKAZU
; TITLE OF INVENTION: IMMUNOSUPPRESSANT
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/636,936
; FILING DATE: 24-APR-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/230,843
; FILING DATE: 21-APR-1994
; APPLICATION NUMBER: JP 094491/1993
; FILING DATE: 21-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 036065/1994
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5856140man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0674-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 729 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: 1..729
US-08-636-936-3
Query Match      11.8%; Score 86; DB 2; Length 729;
Best Local Similarity 100.0%; Pred. No. 1e-33;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 397 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTGCAAGGCTTCTGGTTACTCAATCACT 456

QY 91 GGCTACTACATGCACCTGGGTGAAGCA 116
Db 457 GGCTACTACATGCACCTGGGTGAAGCA 482

RESULT 3
US-08-881-037-11
; Sequence 11, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Glick, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Konski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-037-11
Query Match      9.1%; Score 66; DB 3; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTGCAAGGCTTCTGGTTACTCAATCACT 90
Db 8 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTGCAAGGCTTCTGGTTACTCAATCACT 67

QY 91 GGCTAC 96
Db 68 GGCTAC 73
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Patent No. 620801
GENERAL INFORMATION:
APPLICANT: Ferkol Jr., Thomas W.
APPLICANT: Davis, Pamela B.
APPLICANT: Ziad, Assem-Galal
TITLE OF INVENTION: Serpin Enzyme Complex Receptor -
TITLE OF INVENTION: Mediated Gene Transfer
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,847
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/656,906
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 95/25809
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/216,534
FILING DATE: 23-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: CASE-02280
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 906 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..906
US-09-217-847-24
Query Match 8.6%; Score 63; DB 3; Length 906;
Best Local Similarity 100.0%; Pred. No. 5.6e-22;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CAGCTTCAGCAGCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGC 66
Db 385 CAGCTTCAGCAGCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGC 444
QY 67 AAG 69
Db 445 AAG 447
RESULT 6
US-08-463-128-2
Sequence 2, Application US/08463128
Patent No. 5695755
GENERAL INFORMATION:
APPLICANT: Papayannopoulou, Thalia (USA only)
APPLICANT: Board of Regents, U.
APPLICANT: Washington (except USA)

US-08-656-906-24
Sequence 24, Application US/08656906
Patent No. 5972901
GENERAL INFORMATION:
APPLICANT: Ferkol Jr., Thomas W.
APPLICANT: Davis, Pamela B.
APPLICANT: Ziad, Assem-Galal
TITLE OF INVENTION: Serpin Enzyme Complex Receptor -
TITLE OF INVENTION: Mediated Gene Transfer
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,906
FILING DATE: 03-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 03-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 95/25809
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/216,534
FILING DATE: 23-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: CASE-02280
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 906 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..906
US-08-656-906-24
Query Match 8.6%; Score 63; DB 2; Length 906;
Best Local Similarity 100.0%; Pred. No. 5.6e-22;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CAGCTTCAGCAGCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGC 66
Db 385 CAGCTTCAGCAGCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGC 444
QY 67 AAG 69
Db 445 AAG 447
RESULT 5
US-09-217-847-24
Sequence 24, Application US/09217847

;/ TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
;/ TITLE OF INVENTION: CELLS
;/ NUMBER OF SEQUENCES: 10
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: c/o FISH & NEAVE
;/ STREET: 1251 Avenue of the Americas
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: U.S.A.
;/ ZIP: 10020
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/463,128
;/ FILING DATE: 05-JUN-1995
;/ CLASSIFICATION: 424
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US93/11060
;/ FILING DATE: 11-11-1993
;/ APPLICATION NUMBER: US 07/977,702
;/ FILING DATE: 13-NOV-1992
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Haley Jr., James F.
;/ REGISTRATION NUMBER: 27,794
;/ REFERENCE/DOCKET NUMBER: B173CIP
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (212) 596-9000
;/ TELEFAX: (212) 596-9090
;/ INFORMATION FOR SEQ ID NO: 2:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 318 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-463-128-2

Query Match 8.5%; Score 62; DB 1; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.8e-21;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 ATTCTGCTGTTTTCAGCAGGAGACAGGTTACCATTAACCTGCAAGGCCAGTCAGAGTGT 491
|||
Db 27 ATTCTGCTGTTTTCAGCAGGAGACAGGTTACCATTAACCTGCAAGGCCAGTCAGAGTGT 86
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QY 492 GA 493
|||
Db 87 GA 88

RESULT 7
US-08-463-298-2
;/ Sequence 2, Application US/08463298
;/ Patent No. 5824304
;/ GENERAL INFORMATION:
;/ APPLICANT: Papayannopoulou, Thalia (USA only)
;/ APPLICANT: Board of Regents, U.
;/ APPLICANT: Washington (except USA)
;/ TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
;/ TITLE OF INVENTION: CELLS
;/ NUMBER OF SEQUENCES: 10
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: c/o FISH & NEAVE
;/ STREET: 1251 Avenue of the Americas
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: U.S.A.
;/ ZIP: 10020
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/463,128
;/ FILING DATE: 05-JUN-1995
;/ APPLICATION NUMBER: PCT/US93/11060
;/ FILING DATE: 11-11-1993
;/ APPLICATION NUMBER: US 07/977,702
;/ FILING DATE: 13-NOV-1992

;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/463,298
;/ FILING DATE: 05-JUN-1995
;/ CLASSIFICATION: 424
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US93/11060
;/ FILING DATE: 11-NOV-1993
;/ APPLICATION NUMBER: US 07/977,702
;/ FILING DATE: 13-NOV-1992
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Haley Jr., James F.
;/ REGISTRATION NUMBER: 27,794
;/ REFERENCE/DOCKET NUMBER: B173CIP
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (212) 596-9000
;/ TELEFAX: (212) 596-9090
;/ INFORMATION FOR SEQ ID NO: 2:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 318 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-463-298-2

Query Match 8.5%; Score 62; DB 1; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.8e-21;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 ATTCTGCTGTTTTCAGCAGGAGACAGGTTACCATTAACCTGCAAGGCCAGTCAGAGTGT 491
|||
Db 27 ATTCTGCTGTTTTCAGCAGGAGACAGGTTACCATTAACCTGCAAGGCCAGTCAGAGTGT 86
|||
QY 492 GA 493
|||
Db 87 GA 88

RESULT 8
US-08-436-339A-2
;/ Sequence 2, Application US/08436339A
;/ Patent No. 5843438
;/ GENERAL INFORMATION:
;/ APPLICANT: Papayannopoulou, Thalia (USA only)
;/ APPLICANT: Board of Regents, U.
;/ APPLICANT: Washington (except USA)
;/ TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
;/ TITLE OF INVENTION: CELLS
;/ NUMBER OF SEQUENCES: 10
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: c/o FISH & NEAVE
;/ STREET: 1251 Avenue of the Americas
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: U.S.A.
;/ ZIP: 10020
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/436,339A
;/ FILING DATE:
;/ CLASSIFICATION:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/463,128
;/ FILING DATE: 05-JUN-1995
;/ APPLICATION NUMBER: PCT/US93/11060
;/ FILING DATE: 11-11-1993
;/ APPLICATION NUMBER: US 07/977,702
;/ FILING DATE: 13-NOV-1992


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; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B173CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-436-339A-2
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; Query Match 8.5%; Score 62; DB 2; Length 318;
; Best Local Similarity 100.0%; Pred. No. 1.8e-21;
; Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 432 ATTCCTGCTTTGTTTCAGCAGGAGACAGGGTTACCATACCTGCAAGGCCAGTCAGAGTGT 491
Db 27 ATTCCTGCTTTGTTTCAGCAGGAGACAGGGTTACCATACCTGCAAGGCCAGTCAGAGTGT 86
;
QY 492 GA 493
Db 87 GA 88
;
RESULT 9
US-08-822-830B-3
; Sequence 3, Application US/08822830B
; Patent No. 5871734
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.; Burkly, Linda C.
; TITLE OF INVENTION: Treatment for Asthma with VLA-4 Blocking
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,830B
; FILING DATE: 03-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/456,193
; FILING DATE: 31-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/374,331
; FILING DATE: 18-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/256,631
; FILING DATE: 12-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00030
; FILING DATE: 12-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/821,768
; FILING DATE: 13-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis (PLM)
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: BGP-021USCN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
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; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..318
; OTHER INFORMATION: /note= "HP1/2 light chain variable
; OTHER INFORMATION: chain variable region"
; US-08-822-830B-3
;
; Query Match 8.5%; Score 62; DB 2; Length 318;
; Best Local Similarity 100.0%; Pred. No. 1.8e-21;
; Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 432 ATTCCTGCTTTGTTTCAGCAGGAGACAGGGTTACCATACCTGCAAGGCCAGTCAGAGTGT 491
Db 27 ATTCCTGCTTTGTTTCAGCAGGAGACAGGGTTACCATACCTGCAAGGCCAGTCAGAGTGT 86
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QY 492 GA 493
Db 87 GA 88
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RESULT 10
US-08-950-660-3
; Sequence 3, Application US/08950660
; Patent No. 5932214
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.; Burkly, Linda C.
; TITLE OF INVENTION: Treatment For Inflammatory Bowel Disease
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,660
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/456,124
; FILING DATE:
; APPLICATION NUMBER: US 08/373,857
; FILING DATE: 18-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,603
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00924
; FILING DATE: 02-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/835,139
; FILING DATE: 12-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis (PLM)
; REGISTRATION NUMBER: 35,965
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/ REFERENCE/DOCKET NUMBER: BGP-031USCP2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)227-5941
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 318 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..318
/ OTHER INFORMATION: /note= "HP1/2 light chain variable
/ OTHER INFORMATION: region"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1
/ OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light
/ OTHER INFORMATION: chain variable region"
US-08-950-660-3

Query Match      8.5%; Score 62; DB 2; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.8e-21;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 ATTCTGCTTGTTCAGCAGGAGACAGGGTTACCATACCTGCAAGGCCAGTTCAGAGTGT 491
Db 27 ATTCTGCTTGTTCAGCAGGAGACAGGGTTACCATACCTGCAAGGCCAGTTCAGAGTGT 86

QY 492 GA 493
Db 87 GA 88

RESULT 12
US-08-454-899G-9
; Sequence 9, Application US/08454899G
; Patent No. 6602503
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Tempest, Philip R.
; TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
; FILE REFERENCE: 10274-007001
; CURRENT APPLICATION NUMBER: US/08/454,899G
; CURRENT FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/004,798
; PRIOR FILING DATE: 1993-01-12
; PRIOR APPLICATION NUMBER: PCT/US94/00266
; PRIOR FILING DATE: 1994-01-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain variable region
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(318)
US-08-454-899G-9

Query Match      8.5%; Score 62; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.8e-21;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 ATTCTGCTTGTTCAGCAGGAGACAGGGTTACCATACCTGCAAGGCCAGTTCAGAGTGT 491
Db 27 ATTCTGCTTGTTCAGCAGGAGACAGGGTTACCATACCTGCAAGGCCAGTTCAGAGTGT 86

QY 492 GA 493
Db 87 GA 88

RESULT 13
PCT-US93-00030-3
; Sequence 3, Application PC/TUS9300030
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.
; TITLE OF INVENTION: Treatment for Asthma
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegritti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: PCT/US93/00030
; FILING DATE: 19930112
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 92,307-A; D002 CIP PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..318
; OTHER INFORMATION: /product= "HP1/2 light chain
; OTHER INFORMATION: variable region"
; PCT-US93-00030-3

Query Match      8.5%; Score 62; DB 5; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.8e-21;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 ATTCTGCTGTTGTTTCAGCAGGAGACAGAGGTTTACCATAACCTGCAAGGCCAGTCAGAGTGT 491
Db 27 ATTCTGCTGTTGTTTCAGCAGGAGACAGAGGTTTACCATAACCTGCAAGGCCAGTCAGAGTGT 86

QY 492 GA 493
Db 87 GA 88

RESULT 14
PCT-US93-00924-3
; SEQUENCE 3, Application PC/TUS9300924
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.
; TITLE OF INVENTION: Treatment for Inflammatory Bowel Disease
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00924
; FILING DATE: 19930202
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 92,308-A; D003 CIP PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 3:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..318
; OTHER INFORMATION: /product= "HP1/2 light chain
; OTHER INFORMATION: variable region"
; PCT-US93-00924-3

Query Match      8.5%; Score 62; DB 5; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.8e-21;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 ATTCTGCTGTTGTTTCAGCAGGAGACAGAGGTTTACCATAACCTGCAAGGCCAGTCAGAGTGT 491
Db 27 ATTCTGCTGTTGTTTCAGCAGGAGACAGAGGTTTACCATAACCTGCAAGGCCAGTCAGAGTGT 86

QY 492 GA 493
Db 87 GA 88

RESULT 15
PCT-US94-10395-2
; SEQUENCE 2, Application PC/TUS9410395
; GENERAL INFORMATION:
; APPLICANT: EMORY UNIVERSITY
; APPLICANT: GEORGIA TECH RESEARCH CORPORATION
; APPLICANT: SWERLICK, Robert A.
; APPLICANT: ECKMAN, James R.
; APPLICANT: WICK, Timothy M.
; TITLE OF INVENTION: Method of Inhibiting Binding of
; TITLE OF INVENTION: Reticulocytes to Endothelium by
; TITLE OF INVENTION: Interfering with VLA-4/VCAM-1
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leslie M. Levine
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10395
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,228
; FILING DATE: 15-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Levine, Leslie M.
; REGISTRATION NUMBER: 35,245
; REFERENCE/DOCKET NUMBER: D017CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 252-9810
; TELEFAX: (617) 252-9617
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 318 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US94-10395-2

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Query Match      8.5%; Score 62; DB 5; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.8e-21;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      432 ATTCTGCTTTGTTTCAGCAGGAGACAGGGTTACCATATAACCTGCAAGGCCAGTCAGAGTGT 491
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Db      27 ATTCTGCTTTGTTTCAGCAGGAGACAGGGTTACCATATAACCTGCAAGGCCAGTCAGAGTGT 86

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QY      492 GA 493
      ||
Db      87 GA 88

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Search completed: March 15, 2005, 23:24:20
Job time : 239 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2005, 14:45:28 ; Search time 74 Seconds
(without alignments)
1270.037 Million cell updates/sec

Title: US-10-016-686-1

Perfect score: 1279

Sequence: 1 EVQLQQSGDVLKPGASVKI.....QQDYNSPPTFGGKLEIKR 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 1279 | 100.0 | 243 | 2 | Aaw86002 Murine an |
| 2 | 1279 | 100.0 | 243 | 2 | Aay42294 Anti-5T4 |
| 3 | 1279 | 100.0 | 243 | 2 | Aay27407 5T4 scFv |
| 4 | 1279 | 100.0 | 243 | 4 | Aab83835 Amino aci |
| 5 | 1279 | 100.0 | 592 | 4 | Aab83838 Amino aci |
| 6 | 1279 | 100.0 | 595 | 2 | Aaw86003 Anti-5T4 |
| 7 | 1274 | 99.6 | 488 | 2 | Aaw86004 Human B7- |
| 8 | 1274 | 99.6 | 488 | 2 | Aab83836 Amino aci |
| 9 | 1274 | 99.6 | 488 | 6 | Abu07262 Human exp |
| 10 | 1274 | 99.6 | 488 | 6 | Abu07253 Human exp |
| 11 | 972.5 | 76.0 | 672 | 6 | Abp58454 Engineere |
| 12 | 935 | 73.1 | 267 | 8 | Adf70320 Polioviru |
| 13 | 903.5 | 70.6 | 580 | 2 | Aaw90217 Bispecific |
| 14 | 897.5 | 70.2 | 556 | 2 | Aaw90218 Bispecific |
| 15 | 889.5 | 69.5 | 244 | 8 | Adg17481 Anti-CD22 |
| 16 | 889 | 69.5 | 249 | 1 | Aap80154 Biosynthe |
| 17 | 886.5 | 69.3 | 244 | 8 | Adg17480 Anti-CD22 |
| 18 | 883.5 | 69.1 | 244 | 8 | Adg17477 Anti-CD22 |
| 19 | 883 | 69.0 | 288 | 2 | Aaw82743 Fusion pr |
| 20 | 883 | 69.0 | 673 | 2 | Aaw82742 Plasmid p |
| 21 | 880.5 | 68.8 | 244 | 8 | Adg17482 Anti-CD22 |
| 22 | 880.5 | 68.8 | 244 | 8 | Adg17478 Anti-CD22 |
| 23 | 879 | 68.7 | 895 | 5 | Aau75369 Diphtheri |
| 24 | 879 | 68.7 | 895 | 5 | Aau75368 Diphtheri |
| 25 | 879 | 68.7 | 895 | 5 | Aau75374 Diphtheri |

ALIGNMENTS

RESULT 1

AAW86002

ID AAW86002 standard; protein; 243 AA.

XX

AC AAW86002;

XX 15-MAR-1999 (first entry)

XX Murine anti-5T4 antigen monoclonal antibody scFv.

XX Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;

XX Monoclonal antibody; single chain antibody; scFv; mouse; 5T4scFv.1.

XX Mus sp.

XX Synthetic.

XX Chimeric.

XX Key Location/Qualifiers

FT Misc-difference 169

FT /note= "encoded by GDT"

XX WO9855607-A2.

XX 10-DEC-1998.

XX 04-JUN-1998; 98WO-GB001627.

XX 04-JUN-1997; 97GB-00011579.

XX 20-JUN-1997; 97GB-00013150.

XX 04-JUL-1997; 97GB-00014230.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Kingman SM, Bebbington CR, Ellard PM, Carroll MW, Myers KA;

XX WPI; 1999-059910/05.

XX N-PSDB; AAW80290.

XX New vector encoding a tumour interacting protein for treating cancer - contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat cancer.

XX Example 1; Fig 1A; 82pp; English.

XX This amino acid sequence comprises an scFv, termed 5T4scFv.1, comprising the heavy chain variable region (VH) from the murine 5T4 monoclonal antibody followed by a 15-amino acid flexible linker and the light chain variable region (VL) of the mouse 5T4 antibody. The trophoblast cell

CC surface antigen defined by monoclonal antibody 5T4 is expressed at high
 CC levels on the cells of a wide variety of human tumours. 5T4scFv.1 DNA
 CC (see AAV80290) can be used to construct single-chain antibodies (see
 CC AAW86003) and scFv fusion constructs (see AAW86004-05). The invention
 CC relates to a vector comprising a nucleotide sequence coding for a tumour
 CC interacting protein (TIP) and optionally a nucleotide sequence of
 CC interest (NOI) which encodes a protein of interest (POI), the vector
 CC being capable of delivering the NOI and/or POI to the tumour recognised
 CC by the TIP. Delivery can be in vivo or ex vivo. The vector is used to
 CC treat cancer, and may also be used as a gene delivery system for introducing
 CC at least 1 gene encoding a TIP (preferably a tumour binding protein) into
 CC a haematopoietic cell lineage

XX SQ Sequence 243 AA;

Query Match 100.0%; Score 1279; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 7.5e-84;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLQSGPDLVPGASVKISCKASGYSTFTGYMHVWKQSHGKSLIEWIGRIINPNNGVTLY 60
 DB 1 EVQLQSGPDLVPGASVKISCKASGYSTFTGYMHVWKQSHGKSLIEWIGRIINPNNGVTLY 60

QY 61 NQKFKDKAILTVDKSSTTAYMELSLTSEDSAVYICARSTMTINYYMDYWGQVTSVTSS 120
 DB 61 NQKFKDKAILTVDKSSTTAYMELSLTSEDSAVYICARSTMTINYYMDYWGQVTSVTSS 120

QY 121 GGGSGGGGTGGGSSIVMTQTPTFLVLSAGDRVTITCKASQSVSNVAVYQKPGQSPT 180
 DB 121 GGGSGGGGTGGGSSIVMTQTPTFLVLSAGDRVTITCKASQSVSNVAVYQKPGQSPT 180

QY 181 LLISYTSRYAGVDPDRFIGSGYGTDTFTTISTLQAEADLAVYFCQDYNSPPTFGGKTLE 240
 DB 181 LLISYTSRYAGVDPDRFIGSGYGTDTFTTISTLQAEADLAVYFCQDYNSPPTFGGKTLE 240

QY 241 IKR 243
 DB 241 IKR 243

RESULT 2

AAV42294

ID AAY42294 standard; protein; 243 AA.

XX AC AAY42294;

XX DT 06-DEC-1999 (first entry)

XX DE Anti-5T4 secreted single chain antibody Fv fragment.

XX KW Cytochrome; targeting; localisation; cancer; tumour; produg; reduction;

XX OS nucleus.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO9945127-A2.

XX PD 10-SEP-1999.

XX PF 05-MAR-1999; 99WO-GB000674.

XX PR 06-MAR-1998; 98GB-00004841.

XX PR 19-AUG-1998; 98GB-00018103.

XX PR 29-JAN-1999; 99GB-00002081.

XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.

XX PI Stratford IJ, Patterson AV, Kingman SM, Kan O, Griffiths L;

XX PI Mitrophanous K;

XX DR WPI; 1999-551046/46.

XX DR N-PSDB; AAZ19786.

XX

PT New produg activating agent targeted to selected cells or tissues,

XX particularly hypoxic cells, for treating e.g. tumors.

PS Example 9; Fig 3; 187pp; English.

XX

CC This sequence represents an example of a secreted single chain antibody

CC Fv fragment (in this case, directed against the 5T4 antigen), which is

CC involved in transcellular localisation. A secreted single chain antibody

CC Fv fragment can be fused to cytochrome P450 reductase (P450R) derivatives

CC such as anchorless P450R (AAY42287) or FN fragment (AAY42288). This

CC enables the fusion protein to be delivered to other cells where it is

CC then transported to the nucleus. Many drugs' sites of action are in the

CC nucleus, rather than the cytoplasm, where P450R normally functions. P450R

CC or its derivatives can be used to activate produgs to their active form

CC via reduction. Administration of a produg is useful where the active

CC drug may be metabolised before it reaches its site of action or where the

CC active drug is cytotoxic, e.g., anticancer drugs. Targeted delivery of

CC such produg activators allows a reduction in dose of the produg, and

CC thus of systemic side-effects. P450R derivative fusion proteins, or

CC vectors that express them, are specifically used to treat tumors, or

CC inflammation, atherosclerosis and muscular dystrophy, but may also be

CC used to treat many other conditions, e.g., cerebral malaria, rheumatoid

CC arthritis, or conditions associated with hypoxia, ischaemia or

CC hypoglycemia, or to deliver antibiotics, antiviral agents, analgesics,

CC anaesthetics, anti-inflammatory, antineoplastic agents and diagnostic

CC agents

XX

SQ Sequence 243 AA;

Query Match 100.0%; Score 1279; DB 2; Length 243;

Best Local Similarity 100.0%; Pred. No. 7.5e-84;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLQSGPDLVPGASVKISCKASGYSTFTGYMHVWKQSHGKSLIEWIGRIINPNNGVTLY 60

DB 1 EVQLQSGPDLVPGASVKISCKASGYSTFTGYMHVWKQSHGKSLIEWIGRIINPNNGVTLY 60

QY 61 NQKFKDKAILTVDKSSTTAYMELSLTSEDSAVYICARSTMTINYYMDYWGQVTSVTSS 120

DB 61 NQKFKDKAILTVDKSSTTAYMELSLTSEDSAVYICARSTMTINYYMDYWGQVTSVTSS 120

QY 121 GGGSGGGGTGGGSSIVMTQTPTFLVLSAGDRVTITCKASQSVSNVAVYQKPGQSPT 180

DB 121 GGGSGGGGTGGGSSIVMTQTPTFLVLSAGDRVTITCKASQSVSNVAVYQKPGQSPT 180

QY 181 LLISYTSRYAGVDPDRFIGSGYGTDTFTTISTLQAEADLAVYFCQDYNSPPTFGGKTLE 240

DB 181 LLISYTSRYAGVDPDRFIGSGYGTDTFTTISTLQAEADLAVYFCQDYNSPPTFGGKTLE 240

QY 241 IKR 243

DB 241 IKR 243

RESULT 3

AAV27407

ID AAY27407 standard; protein; 243 AA.

XX AC AAY27407;

XX DT 23-NOV-1999 (first entry)

XX DE 5T4 scFv antibody signal peptide.

XX KW Produg; localization domain; tumor-selective antibody; cytochrome P450;

XX KW Produg activating domain; modified hematopoietic stem cell; MNSC; tumor;

XX KW inflammation; atherosclerosis; muscular dystrophy; cerebral malaria;

XX KW rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; tumor antigen;

XX KW 5T4 scFv.

XX OS Unidentified.

PN WO9945126-A2.
 XX 10-SEP-1999.
 XX
 PF 05-MAR-1999; 99WO-CB000672.
 XX
 PR 06-MAR-1998; 98GB-00004841.
 PR 19-AUG-1998; 98GB-00018103.
 PR 29-JAN-1999; 99GB-00002081.
 XX
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 PI Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;
 PI Mitrophanous K;
 XX
 DR WPI; 1999-540852/45.
 DR N-PSDB; AAZ07810.
 XX
 XX New prodrug activating agent targeted to selected cells or tissues,
 PT particularly hypoxic cells, for treating e.g. tumors or inflammation.
 FT
 XX
 PS Example 9; Fig 3F; 149pp; English.
 XX
 CC The invention provides a new prodrug activating agent that comprises: (i)
 CC a localization domain (LD; other than a tumor-selective antibody) and a
 CC prodrug activating domain (PAD); (ii) at least one nucleic acid encoding
 CC a cytochrome P450 and under control of at least one constitutive or
 CC inducible expression control sequence or (iii) a modified hematopoietic
 CC stem cell (MHSC) containing at least one nucleic acid encoding a PAD and
 CC under control of elements as in (ii). The prodrug activating agent or
 CC vectors that express them, are specifically used to treat tumors,
 CC inflammation, atherosclerosis and muscular dystrophy, but may also be
 CC used to treat many other conditions, e.g. cerebral malaria, rheumatoid
 CC arthritis, or conditions associated with hypoxia, hypoglycemia or
 CC ischemia, or to deliver antibiotics, antiviral agents, analgesics,
 CC anesthetics, anti-inflammatories, antineoplastic agents and diagnostic
 CC agents. LD optimize activity of PAD, e.g. by delivering it to selected
 CC locations or by delivering it to neighboring cells (bystander effect),
 CC and allow a reduction in dose of prodrug, and thus of systemic side-
 CC effects. Nucleic acids encoding the agent may be expressed selectively in
 CC hypoxic cells. The present sequence represents the single chain variable
 CC antibody fragment against the tumor antigen 574 (574 scFv). 574 scFv is
 CC used in the construction of a fusion protein comprising 574 scFv and a
 CC human P450 reductase derivative alp450R
 XX
 SQ Sequence 243 AA;

Query Match 100.0%; Score 1279; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 7.5e-84;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLQQSGPDLVKPGASVKISKASGYSTGYMHWVKQSHGKSLWIGRINPNNGVTLY 60
 |||||
 DB 1 EVQLQQSGPDLVKPGASVKISKASGYSTGYMHWVKQSHGKSLWIGRINPNNGVTLY 60
 |||||

QY 61 NQKFKDKAILTVDKSSTTAYMELRLSTSDSAVYYCARSTMTITNTYMDYWGQVTSVTSS 120
 |||||
 DB 61 NQKFKDKAILTVDKSSTTAYMELRLSTSDSAVYYCARSTMTITNTYMDYWGQVTSVTSS 120
 |||||

QY 121 GGGSGGGGTGGGSSIVMTQTPTLLSAGDRVITCKASQSVSNDAVWYQKPGQSPT 180
 |||||
 DB 121 GGGSGGGGTGGGSSIVMTQTPTLLSAGDRVITCKASQSVSNDAVWYQKPGQSPT 180
 |||||

QY 181 LLISVTSRYAGVPRFRFTGGSGGTGDTFTTISTLQAEALAVYPCQDYNPPFTGGTGLE 240
 |||||
 DB 181 LLISVTSRYAGVPRFRFTGGSGGTGDTFTTISTLQAEALAVYPCQDYNPPFTGGTGLE 240
 |||||

QY 241 IKR 243
 |||||
 DB 241 IKR 243

RESULT 4

AAB83835
 ID AAB83835 standard; protein; 243 AA.
 XX
 AC AAB83835;
 XX
 DT 23-JUL-2001 (first entry)
 XX
 DE Amino acid sequence of a 574 ScFv designated 574ScFv.1.
 XX
 KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
 KW hypersensitivity; autoimmune disease; central nervous system disorder;
 KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
 KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
 KW Helicobacter-related disease; immune disorder.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 169 /note= "Ala encoded by GDT"
 FT
 XX WO200136486-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 13-NOV-2000; 2000WO-GB004317.
 XX
 PR 18-NOV-1999; 99WO-CB003859.
 PR 15-FEB-2000; 2000GB-00003527.
 PR 02-MAR-2000; 2000GB-00005071.
 XX
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 PI Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FW;
 PI Myers KA;
 XX
 DR WPI; 2001-343805/36.
 DR N-PSDB; AAF89729.
 XX
 XX Use of single chain antibody capable of recognizing a disease associated
 PT molecule for manufacturing a medicament for preventing and/or treating a
 PT disease condition associated with disease associated molecule.
 XX
 PS Claim 3; Fig 1; 118pp; English.
 XX
 CC The specification describes the use of a single chain antibody (ScFv),
 CC which is capable of recognizing a disease associated molecule in the
 CC manufacture of a medicament for the prevention and treatment of a disease
 CC condition. The ScFv antibody is useful in the manufacture of a
 CC medicament, for affecting a disease in vivo, for preparing a
 CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
 CC treatment of a disease. The ScFv antibody is also useful for treating
 CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
 CC diseases, cancers, central nervous system disorders including Parkinson's
 CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
 CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
 CC related diseases, and other immune disorders. The present sequence
 CC represents a 574 ScFv of the invention. The antibody comprises the VH and
 CC VL regions from murine 574 monoclonal antibody, joined by a linker
 CC sequence
 XX
 SQ Sequence 243 AA;

Query Match 100.0%; Score 1279; DB 4; Length 243;
 Best Local Similarity 100.0%; Pred. No. 7.5e-84;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLQQSGPDLVKPGASVKISKASGYSTGYMHWVKQSHGKSLWIGRINPNNGVTLY 60
 |||||
 DB 1 EVQLQQSGPDLVKPGASVKISKASGYSTGYMHWVKQSHGKSLWIGRINPNNGVTLY 60
 |||||

QY 61 NQKFKDKAILTVDKSSTTAYMELRLSTSDSAVYYCARSTMTITNTYMDYWGQVTSVTSS 120
 |||||

Db 61 NQFKDKAILTVDKSSTAYMELRSLTSDSAVYCARSTMTITNYVMDYWGQVTSVTYSS 120
QY 121 GGGSGGGGTGGGSSIVMTQTFTFLVSGADRVTITCKASQSVNDVAVYQKPKQSPT 180
Db 121 GGGSGGGGTGGGSSIVMTQTFTFLVSGADRVTITCKASQSVNDVAVYQKPKQSPT 180
QY 181 LLISYTSRYAGVPDRFIGSGYGTDTFTITSLQAEADLAVYFCQDYNPPTFGGTTKLE 240
Db 181 LLISYTSRYAGVPDRFIGSGYGTDTFTITSLQAEADLAVYFCQDYNPPTFGGTTKLE 240
QY 241 IKR 243
Db 241 IKR 243

RESULT 5
AAB83838
ID AAB83838 standard; protein; 592 AA.
XX
AC AAB83838;
XX
DT 23-JUL-2001 (first entry)
XX
DE Amino acid sequence of an Ig-5T4 fusion protein.
XX
KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW hypersensitivity; autoimmune disease; central nervous system disorder;
KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW Helicobacter-related disease; immune disorder.
XX
OS Synthetic.
OS Mus sp.

XX
FH Key Location/Qualifiers
FT Misc-difference 503 /note= "Met encoded by CTC"
FT
XX
PN WO200136486-A2.
XX
PD 25-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-GB004317.
XX
PR 18-NOV-1999; 99WO-GB003859.
PR 15-FEB-2000; 2000GB-00003527.
PR 02-MAR-2000; 2000GB-00005071.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
PI Myers KA;
XX
DR WPI; 2001-343805/36.
DR N-PSDB; AAF89733.
XX
PT Use of single chain antibody capable of recognizing a disease associated
PT molecule for manufacturing a medicament for preventing and/or treating a
PT disease condition associated with disease associated molecule.
XX
PS Disclosure; Fig 6; 118pp; English.

XX
CC The specification describes the use of a single chain antibody (ScFv),
CC which is capable of recognizing a disease associated molecule in the
CC manufacture of a medicament for the prevention and treatment of a disease
CC condition. The ScFv antibody is useful in the manufacture of a
CC medicament, for affecting a disease in vivo, for preparing a
CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC treatment of a disease. The ScFv antibody is also useful for treating
CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC diseases, cancers, central nervous system disorders including Parkinson's
CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular

CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC related diseases, and other immune disorders. The present sequence
CC represents an Ig-5T4 fusion protein
XX
SQ Sequence 592 AA;
Query Match 100.0%; Score 1279; DB 4; Length 592;
Best Local Similarity 100.0%; Pred. No. 2e-83;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLQSGPDLVKGASVKISKASGYSTGYMHWKQSHGKSLGWIGRINPNNGVTLY 60
Db 20 EVQLQSGPDLVKGASVKISKASGYSTGYMHWKQSHGKSLGWIGRINPNNGVTLY 79
QY 61 NQFKDKAILTVDKSSTAYMELRSLTSDSAVYCARSTMTITNYVMDYWGQVTSVTYSS 120
Db 80 NQFKDKAILTVDKSSTAYMELRSLTSDSAVYCARSTMTITNYVMDYWGQVTSVTYSS 139
QY 121 GGGSGGGGTGGGSSIVMTQTFTFLVSGADRVTITCKASQSVNDVAVYQKPKQSPT 180
Db 140 GGGSGGGGTGGGSSIVMTQTFTFLVSGADRVTITCKASQSVNDVAVYQKPKQSPT 199
QY 181 LLISYTSRYAGVPDRFIGSGYGTDTFTITSLQAEADLAVYFCQDYNPPTFGGTTKLE 240
Db 200 LLISYTSRYAGVPDRFIGSGYGTDTFTITSLQAEADLAVYFCQDYNPPTFGGTTKLE 259
QY 241 IKR 243
Db 260 IKR 262

RESULT 6
AAW86003
ID AAW86003 standard; protein; 595 AA.
XX
AC AAW86003;
XX
DT 15-MAR-1999 (first entry)
XX
DE Anti-5T4 single chain antibody 5T4Sabl.
XX
KW Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW monoclonal antibody; single chain antibody; mouse; human; 5T4Sabl.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
PN WO9855607-A2.
XX
PD 10-DEC-1998.
XX
PF 04-JUN-1998; 98WO-GB001627.
XX
PR 04-JUN-1997; 97GB-00011579.
PR 20-JUN-1997; 97GB-00013150.
PR 04-JUL-1997; 97GB-00014230.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
PI WPI; 1999-059910/05.
DR N-PSDB; AAW80291.
XX
PT New vector encoding a tumour interacting protein for treating cancer -
PT contains a desired nucleotide sequence and/or protein which recognises
PT tumours, and is used as a gene delivery system to treat cancer.
XX
PS Example 1; Fig 1B; 82pp; English.
XX
CC This is the amino acid sequence of a single chain antibody (Sabl), termed

OS Homo sapiens.
XX WO200136486-A2.
XX 25-MAY-2001.
XX 13-NOV-2000; 2000WO-GB004317.
XX 18-NOV-1999; 99WO-GB003859.
XX 15-FEB-2000; 2000GB-00003527.
XX 02-MAR-2000; 2000GB-00005071.
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX Kingsman A; Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
XX Myers KA;
XX WPI; 2001-343805/36.
XX N-PSDB; AAF89730.
XX Use of single chain antibody capable of recognizing a disease associated
XX molecule for manufacturing a medicament for preventing and/or treating a
XX disease condition associated with disease associated molecule.
XX Claim 3; Fig 2; 118pp; English.
XX The specification describes the use of a single chain antibody (ScFv),
XX which is capable of recognizing a disease associated molecule in the
XX manufacture of a medicament for the prevention and treatment of a disease
XX condition. The ScFv antibody is useful in the manufacture of a
XX medicament, for affecting a disease in vivo, for preparing a
XX pharmaceutical composition, for in vivo imaging and/or for adjuvant
XX treatment of a disease. The ScFv antibody is also useful for treating
XX inflammatory diseases including arthritis, hypersensitivity, autoimmune
XX diseases, cancers, central nervous system disorders including Parkinson's
XX diseases, periodontal diseases, cardiopulmonary diseases, cardiovascular
XX diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
XX related diseases, and other immune disorders. The present sequence
XX represents a B7-1.5T4.1 fusion protein. This comprises the N-terminus of
XX the 5T4 ScFv is fused after amino acid 215 of human B7-1
XX Sequence 488 AA;
SQ
Query Match 99.6%; Score 1274; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 3.7e-83;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLQSGGPDLVKPGASVKISCKASGYSTGYMHVWVKSHGKSLWIGRINPNNGVTLY 60
DB 247 EVQLQSGGPDLVKPGASVKISCKASGYSTGYMHVWVKSHGKSLWIGRINPNNGVTLY 306
QY 61 NQKFKDKAILTVDKSSTTAYMELSLTSEDSAVYYCARSTMTITNYMDYWGQVTSVTYSS 120
DB 307 NQKFKDKAILTVDKSSTTAYMELSLTSEDSAVYYCARSTMTITNYMDYWGQVTSVTYSS 366
QY 121 GGGSGGGGTGGGGSSIVMTQTPTFLVSGAGRVITTCASQSVSNVDVAVYQKPGQSPT 180
DB 367 GGGSGGGGTGGGGSSIVMTQTPTFLVSGAGRVITTCASQSVSNVDVAVYQKPGQSPT 426
QY 181 LLISYTSRYAGVDPDRFISGGYGTDFETITLQAEEDLAVYFCQDYNPPTFGGKTLE 240
DB 427 LLISYTSRYAGVDPDRFISGGYGTDFETITLQAEEDLAVYFCQDYNPPTFGGKTLE 486
QY 241 IK 242
DB 487 IK 488
RESULT 9
ID ABU07262
XX ABU07262 standard; protein; 488 AA.
XX AC ABU07262;

XX 29-JAN-2003 (first entry)
XX Human expressed protein tag (EPT) #1963.
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX Homo sapiens.
XX WO200278524-A2.
XX 10-OCT-2002.
XX 28-MAR-2002; 2002WO-US009671.
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
XX Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX Example 2; SEQ ID NO 1963; 134pp; English.
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 488 AA;
Query Match 99.6%; Score 1274; DB 6; Length 488;
Best Local Similarity 100.0%; Pred. No. 3.7e-83;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLQSGGPDLVKPGASVKISCKASGYSTGYMHVWVKSHGKSLWIGRINPNNGVTLY 60
DB 247 EVQLQSGGPDLVKPGASVKISCKASGYSTGYMHVWVKSHGKSLWIGRINPNNGVTLY 306
QY 61 NQKFKDKAILTVDKSSTTAYMELSLTSEDSAVYYCARSTMTITNYMDYWGQVTSVTYSS 120
DB 307 NQKFKDKAILTVDKSSTTAYMELSLTSEDSAVYYCARSTMTITNYMDYWGQVTSVTYSS 366
QY 121 GGGSGGGGTGGGGSSIVMTQTPTFLVSGAGRVITTCASQSVSNVDVAVYQKPGQSPT 180
DB 367 GGGSGGGGTGGGGSSIVMTQTPTFLVSGAGRVITTCASQSVSNVDVAVYQKPGQSPT 426
QY 181 LLISYTSRYAGVDPDRFISGGYGTDFETITLQAEEDLAVYFCQDYNPPTFGGKTLE 240
DB 427 LLISYTSRYAGVDPDRFISGGYGTDFETITLQAEEDLAVYFCQDYNPPTFGGKTLE 486
QY 241 IK 242
DB 487 IK 488

Db 367 GGGGGGGTGGGSSIVMTQTPTFLVSAGDRVTITCKASQSVNDVAVYQOKPGQSPT 426

QY 181 LLISYTSRYAGVDRFISGYGTDFTFTISTLQAEADLAVYFCQDYNPPTFGGKTLE 240
 |||||
 Db 427 LLISYTSRYAGVDRFISGYGTDFTFTISTLQAEADLAVYFCQDYNPPTFGGKTLE 486

QY 241 IK 242
 ||
 Db 487 IK 488

RESULT 10

ABU07253

ID ABU07253 standard; protein; 488 AA.

AC ABU07253;

XX

XX

DT 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1954.

DE

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX

OS Homo sapiens.

XX

XX WO200278524-A2.

PN

XX

XX 10-OCT-2002.

PD

XX

XX 28-MAR-2002; 2002WO-US009671.

PF

XX

XX 28-MAR-2001; 2001US-0279495P.

PR

XX 21-MAY-2001; 2001US-0292544P.

PR

XX 08-AUG-2001; 2001US-0310801P.

PR

XX 01-OCT-2001; 2001US-0326370P.

PR

XX 04-DEC-2001; 2001US-0336780P.

PR

XX 20-FEB-2002; 2002US-0358985P.

PR

XX (ZYCO-) ZYCOS INC.

PA

XX Chicx RM, Tomlinson AJ, Urban RG;

PI

XX WPI; 2003-040607/03.

DR

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.

XX

XX Example 2; SEQ ID NO 1954; 134pp; English.

PS

XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 488 AA;

Query Match 99.6%; Score 1274; DB 6; Length 488;
 Best Local Similarity 100.0%; Pred. No. 3.7e-83;
 Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHWVKSHGKSLKLEWIGRINPNNGVTL 60
 |||||
 Db 247 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHWVKSHGKSLKLEWIGRINPNNGVTL 306

QY 61 NOKPKDKAILTVDKSSTTAYMELRLSLTSDSAVYTCARSTMTITNYMDYWGQVTSVTSS 120
 |||||
 Db 307 NOKPKDKAILTVDKSSTTAYMELRLSLTSDSAVYTCARSTMTITNYMDYWGQVTSVTSS 366

QY 121 GGGSGGGGTGGGSSIVMTQTPTFLVSAGDRVTITCKASQSVNDVAVYQOKPGQSPT 180
 |||||
 Db 367 GGGSGGGGTGGGSSIVMTQTPTFLVSAGDRVTITCKASQSVNDVAVYQOKPGQSPT 426

QY 181 LLISYTSRYAGVDRFISGYGTDFTFTISTLQAEADLAVYFCQDYNPPTFGGKTLE 240
 |||||
 Db 427 LLISYTSRYAGVDRFISGYGTDFTFTISTLQAEADLAVYFCQDYNPPTFGGKTLE 486

QY 241 IK 242
 ||
 Db 487 IK 488

RESULT 11

ABP58454

ID ABP58454 standard; protein; 672 AA.

XX

AC ABP58454;

XX

DT 14-APR-2003 (first entry)

XX

XX Engineered superantigen for human cancer therapy.

DE

XX Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
 KW cytostatic; vaccine; human; SEA/E-120; mutant; mutein.
 XX

XX Homo sapiens.

OS Staphylococcus sp.

OS Synthetic.

OS Chimeric.

XX

XX Key Location/Qualifiers

FT Region 1..120

FT /note= "5T4 variable heavy chain"

FT Misc-difference 41

FT /note= "wild-type His substituted by Pro"

FT Misc-difference 44

FT /note= "wild-type Ser substituted by Gly"

FT Misc-difference 69

FT /note= "wild-type Ile substituted by Thr"

FT Misc-difference 113

FT /note= "wild-type Val substituted by Gly"

FT Region 121..222

FT /note= "C242 constant heavy chain"

FT Region 226..458

FT /note= "SEA/E-120"

FT Misc-difference 245

FT /note= "wild-type Arg substituted by Gly"

FT Misc-difference 246

FT /note= "wild-type Asn substituted by Thr"

FT Misc-difference 249

FT /note= "wild-type Ser substituted by Gly"

FT Misc-difference 252

FT /note= "wild-type Arg substituted by Lys"

FT Misc-difference 304

FT /note= "wild-type Lys substituted by Glu"

FT Misc-difference 306

FT /note= "wild-type Lys substituted by Glu"

FT Misc-difference 308

FT /note= "wild-type Lys substituted by Ser"
 FT Misc-difference 309
 FT /note= "wild-type Lys substituted by Ser"
 FT Misc-difference 452
 FT /note= "wild-type Asp substituted by Ser"
 FT Region 459.565
 FT /note= "574 variable light chain"
 FT Misc-difference 469
 FT /note= "wild-type Phe substituted by Ser"
 FT Misc-difference 504
 FT /note= "wild-type Thr substituted by Lys"
 FT Misc-difference 522
 FT /note= "wild-type Ile substituted by Ser"
 FT Misc-difference 532
 FT /note= "wild-type Phe substituted by Leu"
 FT Misc-difference 536
 FT /note= "wild-type Thr substituted by Ser"
 FT Misc-difference 537
 FT /note= "wild-type Leu substituted by Val"
 FT Misc-difference 542
 FT /note= "wild-type Leu substituted by Ala"
 FT Region 566.672
 FT /note= "C242 constant light chain"

XX WO2003002143-A1.

XX 09-JAN-2003.

XX 19-JUN-2002; 2002WO-SE001188.

XX 28-JUN-2001; 2001SE-00002327.

XX (ACTI-) ACTIVE BIOTECH AB.

XX Forsberg G, Erlandsson B, Antonsson P, Walse B;

XX WPI; 2003-201467/19.

XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.

XX Claim 12; Fig 10; 102pp; English.

XX The present sequence is a conjugate of a bacterial superantigen and an
 CC antibody moiety, and has been designed to target and destroy cancer
 CC cells. The bacterial superantigen is SEA/E-120 (see also ABP58455), which
 CC was derived from staphylococcal enterotoxin E (SEE) by the incorporation
 CC of the following amino acid substitutions to reduce seroreactivity whilst
 CC maintaining production levels and biological activity: R20G, N21T, S24G,
 CC R27K, K79E, K81E, K83S and D227S. SEA/E-120 was genetically fused to the
 CC Fab moiety of the tumour reactive antibody 574. Substitutions were made
 CC in the 574 sequence to obtain higher yields: in the heavy chain, H41P,
 CC S44G, I69T and V133G; and in the light chain, F10S, T45K, I63S, F73L,
 CC T77S, L78V and L83A. An expression vector comprising DNA encoding the
 CC conjugate can be used to transform host cells for recombinant production
 CC of the conjugate. The conjugate is useful for treating cancer, including
 CC cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach,
 CC cervix and prostate (claimed)

XX Sequence 672 AA;

Query Match 76.0%; Score 972.5; DB 6; Length 672;
 Best Local Similarity 40.1%; Pred. No. 2.1e-61;
 Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVLOQSGPDLVKPGASVKISKASGYSFTGYMHVWKSHGKSLIEWIGRINPNNGVTLY 60
 DB 1 EVLOQSGPDLVKPGASVKISKASGYSFTGYMHVWKSHGKSLIEWIGRINPNNGVTLY 60
 QY 61 NOKFKDKATLTVDKSTTAYMELRSLTSDSAVYYCARSTMTINTYMDYWGQTSVTVSS 119

Db 61 NOKFKDKATLTVDKSTTAYMELRSLTSDSAVYYCARSTMTINTYMDYWGQTSVTVSS 120
 QY 120 -----
 Db 121 AKTTPPSVYPLAPGSAQAQNSMVTGLGVKGYFPEPVTWNSGSLSSGVHTFPAVLQSD 180
 QY 120 -----
 Db 181 LYTLSSTVTPSSWTWPSETVTCNVAHPASSTKVDKKIIVPRDSGGPSEKSEEINEKDLRKK 240
 QY 120 -----
 Db 123 -----
 Db 241 SELQGTALGNLKOIYYNSKAITSEKSAQDOPLNTLLFKGFTTGHWPWYNLLVDLGSTA 300
 QY 123 -----
 Db 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDKQ 360
 QY 133 -----
 Db 361 TTVPIDKVKTSKKEVTVQELDLQARHLYLHKGFLYNSDSFGGKVQGLIVPHSSSGSTVS 420
 QY 135 -----
 Db 421 YDLFDAQGOYPTLLRIYRDNTTISSTLSISLSLYLTTSIVMTQTFTSLVSAGDRVIT 480
 QY 158 CKASQSVSNDAVWYQKPGQSPPTLLISYTSRYAGVDPDRFTIGSGYGTDTFTTISTLQAD 217
 Db 481 CKASQSVSNDAVWYQKPGQSPPTLLISYTSRYAGVDPDRFTIGSGYGTDTFTTISTLQAD 217
 QY 218 LAVYFCQDYNPPTFTGGTGLEIKR 243
 Db 541 AAVYFCQDYNPPTFTGGTGLEIKR 566
 RESULT 12
 ADR70320
 ID ADR70320 standard; protein; 267 AA.
 AC ADR70320;
 XX 18-NOV-2004 (first entry)
 DE Poliovirus receptor (PVR)-specific scFv2 protein.
 KW poliovirus receptor; PVR; CD155; cluster of differentiation 155;
 KW receptor mediated adhesion modulation;
 KW cell trafficking behaviour modulation;
 KW cell invasion behaviour modulation; proliferative disorder; cancer;
 KW metastasis; PVR-mediated adhesion; PVR-mediated invasion potential;
 KW scFv2.
 OS Unidentified.
 XX WO2004074324-A2.
 XX 02-SEP-2004.
 XX 19-FEB-2004; 2004WO-EP001637.
 XX 24-FEB-2003; 2003US-0450064P.
 XX 28-MAY-2003; 2003EP-00012314.
 XX (XERI-) XERION PHARM AG.
 PA (TUFT) UNIV TUFTS.
 XX Unger CM, Beste G, Zehetmeier C, Lain B, Torella C, Jay DG;
 PI Eustace BK, Sloan KE;
 XX WPI; 2004-652917/63.
 DR N-PSDB; ADR70322.
 XX New molecules that modulate poliovirus receptor (PVR) mediated adhesion,

| | |
|----|--|
| XX | WPI; 2004-062346/06. |
| DR | N-PSDB; ADGI17493. |
| XX | |
| PT | New anti-CD22 antibody having a VH domain and a VL domain comprising at least two amino acid substitutions, useful in diagnosing or treating lymphoma, e.g. B cell non-Hodgkin's lymphoma. |
| PT | |
| XX | |
| XX | Disclosure; SEQ ID NO 6; 66pp; English. |
| PS | |
| CC | The present invention describes a stable anti-CD22 antibody having a VH domain and a VL domain, where the sequences of the VH and VL domains are at least 70% or 90% identical to the sequence of 244 amino acids (ADG17476) and the antibody comprises at least two amino acid substitutions with respect to ADG17476, Gln replacing Glu at position 6, Val replacing Ser at position 12 or Lys replacing Asn at position 62 of the VH domain. Also described: (1) an isolated nucleic acid encoding a stable humanised anti-CD22 antibody described above and that has an L12 binding specificity; (2) an immunoconjugate comprising a stable anti-CD22 antibody described above; (3) a nucleic acid encoding an immunoconjugate of (1); (4) a method of inhibiting growth of a malignant B cell; and (5) a method of detecting a cell that expresses CD22. The anti-CD22 antibody has cytostatic activity. The antibodies are useful in diagnosing or treating lymphoma, e.g. B cell non-Hodgkin's lymphoma. The present invention is used in the exemplification of the present invention. |
| XX | |
| SQ | Sequence 244 AA; |
| | |
| | Query Match 69.5%; Score 889.5; DB 8; Length 244; |
| | Best Local Similarity 69.9%; Pred. No. 6.3e-56; |
| | Matches 174; Conservative 27; Mismatches 37; Indels 11; Gaps 31 |
| Qy | 1 EVQLQQSGPDLVKGPGASVKISCKASGYSTFGYMHVKQSHGKSLIEWIGRINPNNGVTLY 60 |
| Db | 1 QVQLQQSGAELVKGPGASVKMSCKASYTFTSWLHWIKQRPGQGLEWIGYNPRNDYTEY 60 |
| Qy | 61 NQPKDKAILTVDKSSITAYNKLRSLTSEDSAVVYCARSMTIYNMVDWGQVTSVTVSS 120 |
| Db | 61 NQPKDKATLTADKSSSTAYNQLSSLTSEDSAVVYCARRDITT----FYWGQGTTLTAVSS 116 |
| Qy | 121 GGGSGGGGTGGGSSIVMTOTPTFLVLVSAGDRVITTCASQSV-----SNDVAWYQOK 174 |
| Db | 117 GGGSGGGGGGGGSDIVMTQSPSSLVASAGENVMTSCSKSQSVLSYSAHNKNYLAWYQOK 176 |
| Qy | 175 PGQSPTLLISYTSRYAGVPDRFIGSGYGTDFTFTISTLQAEDELAVYPCQDYNSPPFFG 234 |
| Db | 177 PGQSPKLLIYWASTRESGVPRFTGSGSGDTFLTISRVOVEDLAIIYCHQ-YLSSWTFG 235 |
| Qy | 235 GGTGKLEIKR 243 |
| Db | 236 GGTGKLEIKR 244 |

Search completed: March 11, 2005, 14:54:33
Job time : 76 secs

| Result No. | Query | | | DB | ID | Description |
|------------|-------|-------|--------|----|-------------------|-------------------|
| | Score | Match | Length | | | |
| 1 | 883 | 69.0 | 288 | 3 | US-09-423-439-38 | Sequence 38, Appl |
| 2 | 883 | 69.0 | 673 | 3 | US-09-423-439-32 | Sequence 32, Appl |
| 3 | 861 | 67.3 | 249 | 2 | US-08-797-683-18 | Sequence 18, Appl |
| 4 | 861 | 67.3 | 249 | 4 | US-09-984-186-18 | Sequence 18, Appl |
| 5 | 858 | 67.1 | 267 | 4 | US-09-419-788-30 | Sequence 30, Appl |
| 6 | 853 | 66.7 | 260 | 2 | US-08-447-402-1 | Sequence 1, Appl |
| 7 | 848 | 66.3 | 269 | 3 | US-09-070-408-112 | Sequence 132, App |
| 8 | 843.5 | 65.9 | 297 | 4 | US-09-486-814A-2 | Sequence 2, Appl |
| 9 | 839.5 | 65.6 | 240 | 4 | US-10-092-246-35 | Sequence 35, Appl |
| 10 | 838.5 | 65.6 | 240 | 4 | US-10-096-246A-35 | Sequence 35, Appl |
| 11 | 833.5 | 65.2 | 240 | 4 | US-10-092-246-36 | Sequence 36, Appl |
| 12 | 833.5 | 65.2 | 240 | 4 | US-10-096-246A-37 | Sequence 37, Appl |
| 13 | 833.5 | 65.2 | 273 | 2 | US-08-403-853-18 | Sequence 18, Appl |
| 14 | 831.5 | 65.0 | 240 | 4 | US-10-092-246-37 | Sequence 37, Appl |
| 15 | 829 | 64.8 | 244 | 2 | US-08-553-497A-20 | Sequence 20, Appl |
| 16 | 825.5 | 64.5 | 240 | 4 | US-10-096-246A-36 | Sequence 36, Appl |
| 17 | 817 | 63.9 | 246 | 1 | US-08-257-341-7 | Sequence 7, Appl |
| 18 | 817 | 63.9 | 246 | 2 | US-08-553-497A-24 | Sequence 24, Appl |
| 19 | 817 | 63.9 | 252 | 1 | US-08-133-804-4 | Sequence 4, Appl |
| 20 | 817 | 63.9 | 252 | 1 | US-08-461-838-4 | Sequence 4, Appl |
| 21 | 817 | 63.9 | 252 | 2 | US-08-461-386-4 | Sequence 4, Appl |
| 22 | 817 | 63.9 | 367 | 1 | US-08-257-341-5 | Sequence 5, Appl |
| 23 | 814 | 63.6 | 244 | 2 | US-08-553-497A-22 | Sequence 22, Appl |
| 24 | 813.5 | 63.6 | 239 | 3 | US-08-279-772A-8 | Sequence 8, Appl |
| 25 | 813.5 | 63.6 | 239 | 3 | US-08-902-486-11 | Sequence 11, Appl |
| 26 | 813.5 | 63.6 | 599 | 1 | US-08-463-163-3 | Sequence 3, Appl |
| 27 | 813 | 63.6 | 553 | 4 | US-09-203-959A-4 | Sequence 4, Appl |

Db 83 NEKFNKATLTVDKSTTAYMQLSSLTSED SAVYICARERAYGYDDAMDYWGQTTVTS 142
Qy 120 SGGSGSGGGTGGGSSIVMTQTPTFLVSAAGDRAVITTCASQSVND-----VAVYQQ 173
Db 143 SGGSGSGGGTGGGSSIVMTQTPTFLVSAAGDRAVITTCASQSVND-----VAVYQQ 202
Qy 174 KPGQSPKLLIYWASTRSGVDPDRFTGSGSGTDTFTLTSSVQAEDLAIYCKQSY-TLRTF 261
Db 203 RPOQSPKLLIYWASTRSGVDPDRFTGSGSGTDTFTLTSSVQAEDLAIYCKQSY-TLRTF 261
Qy 234 GGGTKLEIKR 243
Db 262 GGGTKLEIKR 271

RESULT 2
US-09-423-439-32
; Sequence 32, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-NO. 6339070-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-423-439-32

Query Match 69.0%; Score 883; DB 3; Length 673;
Best Local Similarity 67.6%; Pred. No. 1.6e-69;
Matches 169; Conservative 38; Mismatches 35; Indels 8; Gaps 3;
Qy 1 EVQLQQSGDPLVKPGASVKISCKASGYFTGYMHVWKQSHGKSLWIGRINPNNGVTLY 60
Db 20 QVQLQQPGHAEVLPKPGASVQLSKASGYFTGYMHVWKQSHGKSLWIGRINPNNGVTLY 79
Qy 61 NQKFKDKAILTVDKSSTTAYMELRLSLSSED SAVYICARSTMI-TNYVMDYWGQVTSVTS 119
Db 80 NEKFNKATLTVDKSTTAYMQLSSLTSED SAVYICARERAYGYDDAMDYWGQTTVTS 139
Qy 120 SGGSGSGGGTGGGSSIVMTQTPTFLVSAAGDRAVITTCASQSVND-----VAVYQQ 173
Db 140 SGGSGSGGGTGGGSSIVMTQTPTFLVSAAGDRAVITTCASQSVND-----VAVYQQ 199
Qy 174 KPGQSPKLLIYWASTRSGVDPDRFTGSGSGTDTFTLTSSVQAEDLAIYCKQSY-TLRTF 261

Db 200 RPOQSPKLLIYWASTRSGVDPDRFTGSGSGTDTFTLTSSVQAEDLAIYCKQSY-TLRTF 258
Qy 234 GGGTKLEIKR 243
Db 259 GGGTKLEIKR 268

RESULT 3
US-08-797-689-18
; Sequence 18, Application US/08797689
; Patent No. 5876969
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; APPLICANT: Fournier, Alain
; APPLICANT: Guittion, Jean-Dominique
; APPLICANT: Jung, Gerard
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-797-689-18

Query Match 67.3%; Score 861; DB 2; Length 249;
Best Local Similarity 67.9%; Pred. No. 3.9e-68;
Matches 167; Conservative 28; Mismatches 47; Indels 4; Gaps 1;
Qy 1 EVQLQQSGDPLVKPGASVKISCKASGYFTGYMHVWKQSHGKSLWIGRINPNNGVTLY 60
Db 4 QVQLQQSGDPLVKPGASVKISCKASGYFTGYMHVWKQSHGKSLWIGRINPNNGVTLY 63
Qy 61 NQKFKDKAILTVDKSSTTAYMELRLSLSSED SAVYICARSTMI-TNYVMDYWGQVTSV 116
Db 64 NGKFKGKATLTADRSSSTAYMQLSSLTSED SAVYICARERAYGYDDAMDYWGQTTV 123
Qy 117 TVSSGGSGGGTGGGSSIVMTQTPTFLVSAAGDRAVITTCASQSVNDVAVYQKPG 176

QY 234 GGGTKLEIKR 243
|||:|
Db 238 GGGTKLEIKR 247

```

RESULT 6
US-08-447-402-1
; Sequence 1, Application US/08447402
; Patent No. 5866344
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent
; APPLICANT: Gevorgian, George
; APPLICANT: Chen, Gang
; TITLE OF INVENTION: IMMUNOASSAY AND ANTIBODY SELECTION
; TITLE OF INVENTION: METHODS USING CELL SURFACE EXPRESSED
; TITLE OF INVENTION: LIBRARIES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433

```

| Query Match | 66.7%; | Score 853; | DB 2; | Length 260; |
|-----------------------|--------------|--|----------------|-------------|
| Best Local Similarity | 66.9%; | Pred. No. 2.1e-47; | | |
| Matches 166; | Conservative | 33; | Mismatches 63; | Indels 6; |
| Gaps 3; | | | | |
| QY | 1 | EVQLQQSGPDLVLPKPGASVKLSCKASQSYFTGYVYHWHVQSHGKSLSEWIGTRINPNNGVTLY | 60 | |
| Ddb | 1 | EVQLQQSGPELVPKPGASVRMSCKSSGIIITDFYMWVRQSHGKSLDYIGYISPSSGVITY | 60 | |
| QY | 61 | NQPKFKALITVDKSSPTAYMELRSLTSDSAVYYCARSTWITNTYVMDYWGQVTSVTVSS | 120 | |
| Ddb | 61 | NQPKFGKATITVDKSSSTAYMELRSLTSDSAVYYCAGSSG-NKWAMDYMGHGASVTVSS | 119 | |
| QY | 121 | GGGSGGGGSGGGGSSIVMTQTPTFLVAGAGDRVITTCCKASQSV---SND---VAVYQOKP | 175 | |
| Ddb | 120 | GGGSGGGGSGGGGSDIVLTQSPASIAVSLGQRATITCRSSQSLVHSGNTYLYNWIYQOKP | 179 | |
| QY | 176 | GQSPFTLLISVTSRYAGVDPDRFICGGYGTDTFTTITLQAEADLAVYFCQDDNSPPTFGG | 235 | |

Db 180 GQPKLLIKVNRFSGVPAFSGSGESDFTLIDPVEEDAAIYCSQTTHVPTFGS 239

```

RESULT 7
US-09-070-408-132
; Sequence 132, Application US/09070408
; Patent No. 6180341
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent L.
; APPLICANT: Georgeou, George
; APPLICANT: Burks, Elizabeth A.
; TITLE OF INVENTION: IN VITRO SCANNING SATURATION MUTAGENESIS
; TITLE OF INVENTION: OF PROTEINS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070.408
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/045,409
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: McMillian, Nabeela R.
; REGISTRATION NUMBER: P-43,363
; REFERENCE/DOCKET NUMBER: UTSB:593
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/447-7577
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-070-408-132

```

[illegible]

QY 236 GTKLEIKR 243
Db 241 GTKLEIIR 248

RESULT 8

US-09-486-814A-2

; Sequence 2, Application US/09486814A
; Patent No. 6562599
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Masato
; APPLICANT: HAYASHI, No. 6562599io
; APPLICANT: YAMAMOTO, Hiroko
; APPLICANT: TOHDOH, Naoki
; TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRUS CORE
; TITLE OF INVENTION: PROTEIN, GENE THEREOF, AND THERAPEUTIC AGENT FOR
; TITLE OF INVENTION: HEPATITIS B CONTAINING THESE
; FILE REFERENCE: 0020-4682P
; CURRENT APPLICATION NUMBER: US/09/486, 814A
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Mus sp., strain: Balb/c, tissue: spleen
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(145)
; OTHER INFORMATION: Identification Method: P
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (177)..(279)
; OTHER INFORMATION: Identification Method: P

US-09-486-814A-2

Query Match 65.9%; Score 843.5; DB 4; Length 297;
Best Local Similarity 67.9%; Pred. No. 1.7e-66;
Matches 167; Conservative 28; Mismatches 42; Indels 9; Gaps 3;
QY 1 EVQLQSGGPDLVKPGASVKISCKASGYFTGYMHVVKSHGKSLWIGRINPNNGVTLY 60
Db 40 QVQLQSGGPELEKPGASVKISCKASGYFTGYNMVKVQSGKSLWIGVITYPNNGTGY 99
QY 61 NQKFKDKAILTVDKSSTAYMELRLSITSEDSAVYYCARSTMTITNYVMYWGQVTSVTSS 120
Db 100 NQKFKSKATLTVDKSSSTAYMQLSLTSEDSAVYYCAR-----LGLDYWGQGTITVTSS 153
QY 121 GGGSGGGGTGGGSSIVMTQTPTFLVLSAGDRVTITCKASQSV-SNDVAVYQKPGQSP 179
Db 154 GGGSGGGSGGGGSDIELTQSPITMAASPGEXITITCSASSSISNLYLHWYQKPGFSP 213
QY 180 TLLISVTSRYAGVPRFRFGSGYGTDTFTTISTLQAEADLVYFCQDYNSPP--TFGGGT 237
Db 214 KLLIYVTSNLASGIPARFSGSGGTSLTIGTMEADVATYCCQGGSSIPRTFGAGT 273
QY 238 KLEIKR 243
Db 274 KLEIKR 279

RESULT 9

US-10-092-246-35

; Sequence 35, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mc
; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007

; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 35
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-35

Query Match 65.6%; Score 839.5; DB 4; Length 240;
Best Local Similarity 66.3%; Pred. No. 2.9e-66;
Matches 161; Conservative 27; Mismatches 50; Indels 5; Gaps 1;
QY 1 EVQLQSGGPDLVKPGASVKISCKASGYFTGYMHVVKSHGKSLWIGRINPNNGVTLY 60
Db 3 QVQLQSGPELVKPGASVKISCKASGYTFTDYHVVHVKPGQGLEWIGTWYPGFDNTY 62
QY 61 NQKFKDKAILTVDKSSTAYMELRLSITSEDSAVYYCARSTMTITNYVMYWGQVTSVTSS 120
Db 63 SETFKGKATLTVDTSNTVYMQLSLTSIEDTAVYFCARGV-----GLDYWGQGTITVTSS 117
QY 121 GGGSGGGGTGGGSSIVMTQTPTFLVLSAGDRVTITCKASQSVSNDVAVYQKPGQSP 180
Db 118 GGGSGGGSGGGGSDIELTQSPKPVVTSIGDIRITCKASQVDVTAAGVYQORPGQSPK 177
QY 181 LLISVTSRYAGVPRFRFGSGYGTDTFTTISTLQAEADLVYFCQDYNSPPTFGGGTGLE 240
Db 178 LLIFWSSTRHTGVPRFRFGSGGTDTFTLISNAQSEDLADYFCHQYSSHPTFTFGSGTGLE 237
QY 241 IKR 243
Db 238 IKR 240

RESULT 10

US-10-096-246A-35
; Sequence 35, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Elaine
; APPLICANT: Nagata, Leslie
; APPLICANT: Alvi, Azhar Z.
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
; TITLE OF INVENTION: Monoclonal ScFv Antibody Against Venezuelan Equine Encephalitis
; TITLE OF INVENTION: Virus (VEE)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/096,246A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 35
; LENGTH: 240
; TYPE: PRT
; ORGANISM: mouse
US-10-096-246A-35

Query Match 65.6%; Score 838.5; DB 4; Length 240;
Best Local Similarity 66.3%; Pred. No. 3.6e-66;
Matches 161; Conservative 27; Mismatches 50; Indels 5; Gaps 1;
QY 1 EVQLQSGGPDLVKPGASVKISCKASGYFTGYMHVVKSHGKSLWIGRINPNNGVTLY 60
Db 3 QVQLQSGPELVKPGASVKISCKASGYTFTDYHVVHVKPGQGLEWIGTWYPGFDNTY 62
QY 61 NQKFKDKAILTVDKSSTAYMELRLSITSEDSAVYYCARSTMTITNYVMYWGQVTSVTSS 120
Db 63 SETFKGKATLTVDTSNTVYMQLSLTSIEDTAVYFCARGV-----GLDYWGQGTITVTSS 117
QY 121 GGGSGGGGTGGGSSIVMTQTPTFLVLSAGDRVTITCKASQSVSNDVAVYQKPGQSP 180
Db 118 GGGSGGGSGGGGSDIELTQSPKPVVTSIGDIRITCKASQVDVTAAGVYQORPGQSPK 177


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; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-403-853-18

Query Match 65.2%; Score 833.5; DB 2; Length 273;
Best Local Similarity 67.2%; Pred. No. 1.2e-65;
Matches 164; Conservative 26; Mismatches 51; Indels 3; Gaps 2;

QY 1 EVLOQSGPDLVKPGASVKISKASGYFTGYMHVVKSHGKSLWIGRINPNNGVTLY 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
23 QVOLQSGAELVKPGASVRMSCKASGYFTTNMYVMVKSPGGLWIGIFYPGNGDTSY 82
QY 61 NOKPKDKALLVDKSTTAYMELRSLTSDSAVYICARSTMTINY--VMDYWGQVTSVTV 118
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
83 NOKPKDKALLVDKSTTAYMELRSLTSDSAVYICARSTMTINY--VMDYWGQVTSVTV 142
QY 119 SSGGGGGGGGGGGGGSSIVMTQPTFLVLSAGDRVTITCKASQSVNDVAVYQKPGOS 178
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
143 -SGGGGGGGGGGGGGSSIVMTQPTFLVLSAGDRVTITCKASQSVNDVAVYQKPGOS 201
QY 179 PTLISYTSRYAGVDPDRFTGSGYGTDTFTTISTLQAEADLAVYFCQDYNPPTFGGKTK 238
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
202 VKLLIYTSNLHSEVPSRSGSGGTDYSLTISNLEQEDIATYFCQDFTLPTFGGKTK 261
QY 239 LEIK 242
Db :||||:
262 LEIR 265

RESULT 14
US-10-092-246-37
; Sequence 37, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of M
; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092, 246
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-37

Query Match 65.0%; Score 831.5; DB 4; Length 240;
Best Local Similarity 65.8%; Pred. No. 1.5e-65;
Matches 160; Conservative 27; Mismatches 51; Indels 5; Gaps 1;

QY 1 EVLOQSGPDLVKPGASVKISKASGYFTGYMHVVKSHGKSLWIGRINPNNGVTLY 60
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3 QVOLQSGPDLVKPGASVKISKASGYFTDHYHVMVKSPGGLWIGMTYFGPDNTY 62
QY 61 NOKPKDKALLVDKSTTAYMELRSLTSDSAVYICARSTMTINYMDYWGQVTSVTSS 120
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
63 SETFGKATLTVDTSNTVYMLSSLTSDTAVYFCARGV-----GLDYWGQGTIVTSS 117
QY 121 GGGGGGGGGGGGGSSIVMTQPTFLVLSAGDRVTITCKASQSVNDVAVYQKPGOSPT 180
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
118 GGGGGGGGGGGGGSSIVMTQPTFLVLSAGDRVTITCKASQSVNDVAVYQKPGOSPK 177

; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-403-853-18

Query Match 65.2%; Score 833.5; DB 2; Length 273;
Best Local Similarity 67.2%; Pred. No. 1.2e-65;
Matches 164; Conservative 26; Mismatches 51; Indels 3; Gaps 2;

QY 1 EVLOQSGPDLVKPGASVKISKASGYFTGYMHVVKSHGKSLWIGRINPNNGVTLY 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
23 QVOLQSGAELVKPGASVRMSCKASGYFTTNMYVMVKSPGGLWIGIFYPGNGDTSY 82
QY 61 NOKPKDKALLVDKSTTAYMELRSLTSDSAVYICARSTMTINY--VMDYWGQVTSVTV 118
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
83 NOKPKDKALLVDKSTTAYMELRSLTSDSAVYICARSTMTINY--VMDYWGQVTSVTV 142
QY 119 SSGGGGGGGGGGGGGSSIVMTQPTFLVLSAGDRVTITCKASQSVNDVAVYQKPGOS 178
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
143 -SGGGGGGGGGGGGGSSIVMTQPTFLVLSAGDRVTITCKASQSVNDVAVYQKPGOS 201
QY 179 PTLISYTSRYAGVDPDRFTGSGYGTDTFTTISTLQAEADLAVYFCQDYNPPTFGGKTK 238
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
202 VKLLIYTSNLHSEVPSRSGSGGTDYSLTISNLEQEDIATYFCQDFTLPTFGGKTK 261
QY 239 LEIK 242
Db :||||:
262 LEIR 265

RESULT 15
US-08-553-497A-20
; Sequence 20, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLEBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSOW, DETLEF
; APPLICANT: ADAN, JAUME
; APPLICANT: MITJANS, FRANCESC
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PITULATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSER: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-553-497A-20

Query Match 64.8%; Score 829; DB 2; Length 244;
Best Local Similarity 66.9%; Pred. No. 2.5e-65;
Matches 164; Conservative 27; Mismatches 50; Indels 4; Gaps 3;

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Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 EVLOQSGAELVKPGASVKLSCKASGYFTTSHMHWVKQRAGGLEWIGFNPNGRTNY 60
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| Db | 61 | NEKFKDKAILTVDKSSTAYMEILRSITSEDSAVYYCASRDYDYGRIYFDYWGQGITVTYS | 120 |
| QY | 120 | SGGGSGGGGTGGGSSIVMTQTFFLLYSAGDRVTITCKASOSVSNVDVAVYQOKPQSP | 179 |
| Db | 121 | SGGGSGGGGTGGGSDIELTQSPAIMSASPGKVTWTCASSSVSY-MYWIQOKPQSSP | 179 |
| QY | 180 | TLIISYTSRYAGVPRFIGSGYGTDTFTTISTLQAEIDLAVFCQODYNSPP--TFGGGT | 237 |
| Db | 180 | RLIYDTSNLAGVPRVRFSGSGGTSYSLTISRMEADAATYCCQOWSSVPPMYTFGGGT | 239 |
| QY | 238 | KLEIK | 242 |
| Db | 240 | KLEIK | 244 |

Search completed: March 11, 2005, 14:56:32
Job time : 24 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2005, 14:55:53 ; Search time 137 Seconds
(without alignments)
585.053 Million cell updates/sec

Title: US-10-016-686-1

Perfect score: 1279

Sequence: 1 EVQLQQSGPLVKPGASVKI.....QQDYNSPPTFGGKLEIKR 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/ECT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 1279 | 100.0 | 243 | 16 | US-10-334-235-37 |
| 2 | 1279 | 100.0 | 600 | 16 | Sequence 37, Appl |
| 3 | 1274 | 99.6 | 488 | 16 | Sequence 38, Appl |
| 4 | 994 | 77.7 | 243 | 17 | US-10-334-235-39 |
| 5 | 972.5 | 76.0 | 672 | 10 | Sequence 39, Appl |
| 6 | 909 | 71.1 | 331 | 14 | Sequence 10, Appl |
| 7 | 879 | 68.7 | 895 | 16 | Sequence 11, Appl |
| 8 | 879 | 68.7 | 895 | 16 | Sequence 169, App |
| 9 | 879 | 68.7 | 895 | 16 | US-10-059-281-169 |
| 10 | 879 | 68.7 | 895 | 16 | US-10-296-085A-19 |
| 11 | 879 | 68.7 | 895 | 17 | US-10-296-085A-20 |
| 12 | 879 | 68.7 | 895 | 17 | US-10-296-085A-27 |
| 13 | 879 | 68.7 | 896 | 16 | Sequence 27, Appl |
| | | | | | Sequence 4, Appli |
| | | | | | Sequence 17, Appl |
| | | | | | Sequence 18, Appl |
| | | | | | Sequence 26, Appl |

| | | | | | | |
|----|-------|------|-----|----|--------------------|-------------------|
| 14 | 879 | 68.7 | 896 | 17 | US-10-496-179-2 | Sequence 2, Appli |
| 15 | 879 | 68.7 | 896 | 17 | US-10-496-179-3 | Sequence 3, Appli |
| 16 | 879 | 68.7 | 896 | 17 | US-10-496-179-7 | Sequence 7, Appli |
| 17 | 879 | 68.7 | 899 | 16 | US-10-296-085A-28 | Sequence 28, Appl |
| 18 | 879 | 68.7 | 899 | 17 | US-10-496-179-5 | Sequence 2, Appli |
| 19 | 870 | 68.0 | 631 | 15 | US-10-120-198B-2 | Sequence 2, Appli |
| 20 | 869.5 | 68.0 | 264 | 14 | US-10-114-716A-46 | Sequence 46, Appl |
| 21 | 861 | 67.3 | 249 | 9 | US-09-984-186-18 | Sequence 18, Appl |
| 22 | 861 | 67.3 | 249 | 14 | US-10-237-667-18 | Sequence 18, Appl |
| 23 | 861 | 67.3 | 249 | 14 | US-10-237-708-18 | Sequence 18, Appl |
| 24 | 861 | 67.3 | 249 | 14 | US-10-237-866-18 | Sequence 18, Appl |
| 25 | 861 | 67.3 | 249 | 14 | US-10-237-871-18 | Sequence 18, Appl |
| 26 | 861 | 67.3 | 249 | 14 | US-10-237-624-18 | Sequence 18, Appl |
| 27 | 861 | 67.3 | 249 | 15 | US-10-702-536-18 | Sequence 18, Appl |
| 28 | 861 | 67.3 | 249 | 15 | US-10-702-636-18 | Sequence 18, Appl |
| 29 | 853 | 66.7 | 260 | 10 | US-09-782-672-2 | Sequence 2, Appli |
| 30 | 853 | 66.7 | 260 | 10 | US-09-782-671B-2 | Sequence 2, Appli |
| 31 | 853 | 66.7 | 260 | 11 | US-09-813-444-2 | Sequence 2, Appli |
| 32 | 841 | 65.8 | 258 | 15 | US-10-239-656-59 | Sequence 59, Appl |
| 33 | 839.5 | 65.6 | 240 | 14 | US-10-096-246-35 | Sequence 35, Appl |
| 34 | 833.5 | 65.2 | 240 | 14 | US-10-096-246-36 | Sequence 36, Appl |
| 35 | 833.5 | 65.2 | 622 | 15 | US-10-378-832A-2 | Sequence 2, Appli |
| 36 | 832 | 65.1 | 249 | 10 | US-09-880-748-1635 | Sequence 1635, Ap |
| 37 | 832 | 65.1 | 249 | 15 | US-10-293-418-1635 | Sequence 1635, Ap |
| 38 | 831.5 | 65.0 | 240 | 14 | US-10-096-246-37 | Sequence 37, Appl |
| 39 | 830.5 | 64.9 | 242 | 14 | US-10-259-087A-20 | Sequence 20, Appl |
| 40 | 830.5 | 64.9 | 242 | 16 | US-10-689-006-20 | Sequence 20, Appl |
| 41 | 830.5 | 64.9 | 248 | 17 | US-10-879-994-14 | Sequence 14, Appl |
| 42 | 829.5 | 64.9 | 248 | 10 | US-09-880-748-1104 | Sequence 1104, Ap |
| 43 | 828.5 | 64.9 | 248 | 15 | US-10-293-418-1104 | Sequence 1104, Ap |
| 44 | 825 | 64.5 | 245 | 14 | US-10-138-505-40 | Sequence 40, Appl |
| 45 | 825 | 64.5 | 245 | 15 | US-10-257-864A-95 | Sequence 95, Appl |

ALIGNMENTS

RESULT 1
US-10-334-235-37
; Sequence 37, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingsman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Cartoll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingsman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 532682000920
; CURRENT APPLICATION NUMBER: US/10/334,235
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: mature secreted protein of 5T4 scFv, designated
; OTHER INFORMATION: 5T4scFv.1
US-10-334-235-37

Query Match 100.0%; Score 1279; DB 16; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.1e-89;

APPLICANT: Karow, Margaret
APPLICANT: Smith, Eric
TITLE OF INVENTION: HIGH AFFINITY FUSION PROTEINS AND THERAPEUTIC AND DIAGNOSTIC METH
TITLE OF INVENTION: USE
FILE REFERENCE: REG 203E2
CURRENT APPLICATION NUMBER: US/10/879,994
CURRENT FILING DATE: 2004-06-29
PRIOR APPLICATION NUMBER: 10/610,452
PRIOR FILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 243
TYPE: PRT
ORGANISM: mus musculus
US-10-879-994-10

Query Match 77.7%; Score 994; DB 17; Length 243;
Best Local Similarity 78.7%; Pred. No. 5.7e-68;
Matches 192; Conservative 19; Mismatches 31; Indels 2; Gaps 2;

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DB 1 QVQLQSGAELAKPGASVKISCKASGYSTGYMHVWIKORPGGLEWIGYINPSTGYSEF 60
QY 61 NQKFKDKAILTVDKSSTAYMELRLSTSEDSAVYYCARSTMITNYMVDYMGQVTSVTSS 120
DB 61 NQKFNDAKATLADRSSTAYMQLNSLTSEDSAVYYCARDAYGNY-EDYMGQGTTLTVSS 119
QY 121 -GGGSGGGGTGGGSSIVMTQPTPELLVSAGDRVTITCKASQSVNDVAVYQKPGQSP 179
DB 120 AGGSGGGGGGGGGSSIVMTQPTPELLVSAGDRVTITCKASQSVNDVAVYQKPGQSP 179
QY 180 TLLISYTSRYAGVPRFRFGTGGVGTDTFTTISTLQAEADLVYFCQDYNPPTFGGKTL 239
DB 180 KLIYIESNRKSGVPRFRFGTGGNGDTFTTISTVQAEADLVYFCQVYTSPTFGGKTL 239
QY 240 EIKR 243
DB 240 EIKR 243

RESULT 5
US-09-900-766-1
Sequence 1, Application US/09900766
Publication No. US2003003965A1
GENERAL INFORMATION:
APPLICANT: FORSBERG, GORAN
APPLICANT: ERLANDSSON, EVA
APPLICANT: ANTONSSON, PER
APPLICANT: WALSE, BJORN
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
FILE REFERENCE: P02188U0;10104199
CURRENT APPLICATION NUMBER: US/09/900,766
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 672
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)-(672)
OTHER INFORMATION: Conjugate protein
US-09-900-766-1

Query Match 76.0%; Score 972.5; DB:10; Length 672;
Best Local Similarity 40.1%; Pred. No. 7.2e-66;
Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHVWVKQSGKLEWIGRINPNNGVTLY 60
|||||

DB 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHVWVKQSGKLEWIGRINPNNGVTLY 60
QY 61 NQKFKDKAILTVDKSSTAYMELRLSTSEDSAVYYCARSTMITNYMVDYMGQVTSVTSS- 119
|||||
DB 61 NQKFKDKAILTVDKSSTAYMELRLSTSEDSAVYYCARSTMITNYMVDYMGQVTSVTSS 120
QY 120 ----- 119
DB 121 AKTTPPSVYPLAGSAAQTNSMVLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180
QY 120 -----SGG----- 122
DB 181 LYTLSSTVTPSSVTPSETVTCNVAHPASSVKDKKIVPRDSGGPSEKSEBINEKDLRKK 240
QY 123 ----- 122
DB 241 SELQGTALGNLQIYYVNSKAITSEKSAQDLTNTLLFKGPFTHGHPWYNLDLVLGSTA 300
QY 123 -----GGSGGGT----- 132
DB 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLTEEKVPINLWIDGKQ 360
QY 133 -----GG----- 134
DB 361 TVPIDKVKTSKKEVTVOELDQARHLYHGKPLGYNSSDFGKQVQGLIVFHSSEGSTVS 420
QY 135 -----SSIVMTQPTPELLVSAGDRVTIT 157
DB 421 YDLFDAQGYPTLLRIYRDNTTISSTLSLSLYLVTTSIVMTQPTPELLVSAGDRVTIT 480
QY 158 CKASQSVNDVAVYQKPGQSPPELLISYTSRYAGVPRFRFGSGYGTDTFTTISTLQAEAD 217
DB 481 CKASQSVNDVAVYQKPGQSPPELLISYTSRYAGVPRFRFGSGYGTDTFTTISTLQAEAD 540
QY 218 LAVYFCQDYNPPTFGGKLEIKR 243
DB 541 AAVYFCQDYNPPTFGGKLEIKR 566

RESULT 6
US-10-059-261-169
Sequence 169, Application US/10059261
Publication No. US20030077826A1
GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: BRIAND, JEAN-PAUL
APPLICANT: ETIENNE DANIEL FRANCOIS
TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC
TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
FILE REFERENCE: 03495.0216
CURRENT APPLICATION NUMBER: US/10/059,261
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/265,594
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 325
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 169
LENGTH: 331
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: vector pACgp67-scfv350
US-10-059-261-169

Query Match 71.1%; Score 909; DB 14; Length 331;
Best Local Similarity 70.4%; Pred. No. 2.3e-61;
Matches 171; Conservative 28; Mismatches 42; Indels 2; Gaps 1;

QY 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHVWVKQSGKLEWIGRINPNNGVTLY 60
|||||

Db 86 QVLOQSGABELAKPGASVKLCKASGHTFTSYMHVWKQPGGLEWIGYINLSSGIYKI 145
QY 61 NQFKDKAILTVDKSSTTAYMELRSLTSEDSAVYICARSTMTITNYVMDYWGQVTSVTSS 120
Db 146 NQFKDKAILTVDKSSTTAYMELRSLTSEDSAVYICARSTMTITNYVMDYWGQVTSVTSS 203
QY 121 GGGSGGGGGGGGGSSIVMTQPTFTLLVSGDRVTITCKASQSVNDVAVYQKPGQSPT 180
Db 204 GGGSGGGGGGGGGSSIVMTQPTFTLLVSGDRVTITCKASQSVNDVAVYQKPGQSPT 263
QY 181 LLLSYTSRVRAGVDPDRFPGSGYGTDTFTTISTLOAEDLAVYFCQDYNSPPTFGGTTKLE 240
Db 264 LLLSYTSRVRAGVDPDRFPGSGYGTDTFTTISTLOAEDLAVYFCQDYNSPPTFGGTTKLE 323
QY 241 IKR 243
Db 324 IKR 326

RESULT 7
US-10-296-085A-19
; Sequence 19, Application US/10296085A
; Publication No. US20040127682A1
; GENERAL INFORMATION:
; APPLICANT: DAVID M. NEVILLE
; APPLICANT: JERRY T. THOMPSON
; APPLICANT: JUNG-HEE WOO
; APPLICANT: HUAIZHONG HU
; APPLICANT: SHENGLIN MA
; APPLICANT: JONATHAN MARK HEXHAM
; APPLICANT: MARY ELLEN DIGAN
; TITLE OF INVENTION: IMMUNOTOXIN FUSION PROTEINS AND MEANS
; FILE REFERENCE: 14028.0294U2
; CURRENT APPLICATION NUMBER: US/10/296, 085A
; CURRENT FILING DATE: 2002-11-18
; PRIOR FILING DATE: 2000-05-18
; PRIOR FILING DATE: 1999-09-03
; PRIOR FILING DATE: 1996-10-29
; PRIOR FILING DATE: 1997-03-05
; PRIOR FILING DATE: 1995-10-30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 895
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence/Note =
; OTHER INFORMATION: synthetic construct
US-10-296-085A-19

Query Match 68.7%; Score 879; DB 16; Length 895;
Best Local Similarity 70.1%; Pred. No. 1.3e-58;
Matches 171; Conservative 25; Mismatches 46; Indels 2; Gaps 1;
QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWKQSHGKSLIEWIGRINPNNGVTLY 60
Db 515 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWKQSHGKSLIEWIGRINPNNGVTLY 574
QY 61 NQFKDKAILTVDKSSTTAYMELRSLTSEDSAVYICARSTMTITNYVMDYWGQVTSVTV 118
Db 575 NQFKDKAILTVDKSSTTAYMELRSLTSEDSAVYICARSTMTITNYVMDYWGQVTSVTV 634

QY 119 SSGGGGGGGGGGGSSIVMTQPTFTLLVSGDRVTITCKASQSVNDVAVYQKPGQS 178
Db 635 SSGGGGGGGGGGGSSIVMTQPTFTLLVSGDRVTITCKASQSVNDVAVYQKPGQS 694
QY 179 PTLISYTSRVRAGVDPDRFPGSGYGTDTFTTISTLOAEDLAVYFCQDYNSPPTFGGTTK 238
Db 695 VKLLIYTSRHLGSHVPSKPSGSGGSDYSLTISLEQEDLATYFCQDQNTLPTWTFAGGTTK 754
QY 239 LEIK 242
Db 755 LEIK 758

RESULT 8
US-10-296-085A-20
; Sequence 20, Application US/10296085A
; Publication No. US20040127682A1
; GENERAL INFORMATION:
; APPLICANT: DAVID M. NEVILLE
; APPLICANT: JERRY T. THOMPSON
; APPLICANT: JUNG-HEE WOO
; APPLICANT: HUAIZHONG HU
; APPLICANT: SHENGLIN MA
; APPLICANT: JONATHAN MARK HEXHAM
; APPLICANT: MARY ELLEN DIGAN
; TITLE OF INVENTION: IMMUNOTOXIN FUSION PROTEINS AND MEANS
; FILE REFERENCE: 14028.0294U2
; CURRENT APPLICATION NUMBER: US/10/296, 085A
; CURRENT FILING DATE: 2002-11-18
; PRIOR FILING DATE: 2000-05-18
; PRIOR FILING DATE: 1999-09-03
; PRIOR FILING DATE: 1996-10-29
; PRIOR FILING DATE: 1997-03-05
; PRIOR FILING DATE: 1995-10-30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 895
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence/Note =
; OTHER INFORMATION: synthetic construct
US-10-296-085A-20

Query Match 68.7%; Score 879; DB 16; Length 895;
Best Local Similarity 70.1%; Pred. No. 1.3e-58;
Matches 171; Conservative 25; Mismatches 46; Indels 2; Gaps 1;
QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWKQSHGKSLIEWIGRINPNNGVTLY 60
Db 515 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWKQSHGKSLIEWIGRINPNNGVTLY 574
QY 61 NQFKDKAILTVDKSSTTAYMELRSLTSEDSAVYICARSTMTITNYVMDYWGQVTSVTV 118
Db 575 NQFKDKAILTVDKSSTTAYMELRSLTSEDSAVYICARSTMTITNYVMDYWGQVTSVTV 634
QY 119 SSGGGGGGGGGGGSSIVMTQPTFTLLVSGDRVTITCKASQSVNDVAVYQKPGQS 178
Db 635 SSGGGGGGGGGGGSSIVMTQPTFTLLVSGDRVTITCKASQSVNDVAVYQKPGQS 694
QY 179 PTLISYTSRVRAGVDPDRFPGSGYGTDTFTTISTLOAEDLAVYFCQDYNSPPTFGGTTK 238

; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 09/389,565
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/US98/04303
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: 08/739,703
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/039,987
; PRIOR FILING DATE: 1997-03-05
; PRIOR APPLICATION NUMBER: 60/008,104
; PRIOR FILING DATE: 1995-10-30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 896
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: synthetic construct
US-10-296-085A-17

Query Match 68.7%; Score 879; DB 16; Length 896;
Best Local Similarity 70.1%; Pred. No. 1.3e-58;
Matches 171; Conservative 25; Mismatches 46; Indels 2; Gaps 1;
QY 1 EVLOQSGPDLVKPGASVKISKASGYSTGYTHMVKQSHGKSLWIGRIINPNNGVTLV 60
DB 516 EVLOQSGPELVKPGASMKISKASGYSTGYTMNWKQSHGKNLEWMLINPYKGVSTY 575
QY 61 NQKFKDKAILTVDKSSTTAYMELRLSITSDSAVYICARSTMI--TNYVMDYMGQVTSVT 118
DB 576 NQKFKDKATLVDKSSSTAYMELLSITSDSAVYICARSGYSDSWYFDVWGAGTTTV 635
QY 119 SSGGGSGGGTGGGSSIVMTQPTFLVSGAGDRVTITCKASQSVNSDVAVYQKPGQS 178
DB 636 SSGGGSGGGGSGGGSDIQMTQTSSLSASLGDRVTISCRASQDIRNLNLYQKPDGT 695
QY 179 PTLISYTSRYAGVDPDRFGSGYGTDFTTISLQAEADVYFCQDYNSPPTFGGK 238
DB 696 VKLLIYTSRLHSGVSPKSGSGSDYSLTISNLEQEDIATYFCQGNLTLPWTFAGGK 755
QY 239 LEIK 242
DB 756 LEIK 759

RESULT 12
US-10-296-085A-18
; Sequence 18, Application US/10296085A
; Publication No. US20040127682A1
; GENERAL INFORMATION:
; APPLICANT: DAVID M. NEVILLE
; APPLICANT: JERRY T. THOMPSON
; APPLICANT: JUNG-HEE WOO
; APPLICANT: HUAIZHONG HU
; APPLICANT: SHENGLIN MA
; APPLICANT: JONATHAN MARK HEXHAM
; APPLICANT: MARY ELLEN DIGAN
; TITLE OF INVENTION: IMMUNOTOXIN FUSION PROTEINS AND MEANS
; FILE REFERENCE: 14028.0294U2
; CURRENT APPLICATION NUMBER: US/10/296,085A
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/573,797
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/380,484
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 09/389,565
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/US98/04303
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: 08/739,703

; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/039,987
; PRIOR FILING DATE: 1997-03-05
; PRIOR APPLICATION NUMBER: 60/008,104
; PRIOR FILING DATE: 1995-10-30
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 896
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: synthetic construct
US-10-296-085A-18

Query Match 68.7%; Score 879; DB 16; Length 896;
Best Local Similarity 70.1%; Pred. No. 1.3e-58;
Matches 171; Conservative 25; Mismatches 46; Indels 2; Gaps 1;
QY 1 EVLOQSGPDLVKPGASVKISKASGYSTGYTHMVKQSHGKSLWIGRIINPNNGVTLV 60
DB 516 EVLOQSGPELVKPGASMKISKASGYSTGYTMNWKQSHGKNLEWMLINPYKGVSTY 575
QY 61 NQKFKDKAILTVDKSSTTAYMELRLSITSDSAVYICARSTMI--TNYVMDYMGQVTSVT 118
DB 576 NQKFKDKATLVDKSSSTAYMELLSITSDSAVYICARSGYSDSWYFDVWGAGTTTV 635
QY 119 SSGGGSGGGTGGGSSIVMTQPTFLVSGAGDRVTITCKASQSVNSDVAVYQKPGQS 178
DB 636 SSGGGSGGGGSGGGSDIQMTQTSSLSASLGDRVTISCRASQDIRNLNLYQKPDGT 695
QY 179 PTLISYTSRYAGVDPDRFGSGYGTDFTTISLQAEADVYFCQDYNSPPTFGGK 238
DB 696 VKLLIYTSRLHSGVSPKSGSGSDYSLTISNLEQEDIATYFCQGNLTLPWTFAGGK 755
QY 239 LEIK 242
DB 756 LEIK 759

RESULT 13
US-10-296-085A-26
; Sequence 26, Application US/10296085A
; Publication No. US20040127682A1
; GENERAL INFORMATION:
; APPLICANT: DAVID M. NEVILLE
; APPLICANT: JERRY T. THOMPSON
; APPLICANT: JUNG-HEE WOO
; APPLICANT: HUAIZHONG HU
; APPLICANT: SHENGLIN MA
; APPLICANT: JONATHAN MARK HEXHAM
; APPLICANT: MARY ELLEN DIGAN
; TITLE OF INVENTION: IMMUNOTOXIN FUSION PROTEINS AND MEANS
; FILE REFERENCE: 14028.0294U2
; CURRENT APPLICATION NUMBER: US/10/296,085A
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/573,797
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/380,484
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 09/389,565
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/US98/04303
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: 08/739,703
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/039,987
; PRIOR FILING DATE: 1997-03-05
; PRIOR APPLICATION NUMBER: 60/008,104
; PRIOR FILING DATE: 1995-10-30
; NUMBER OF SEQ ID NOS: 122

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 896
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: synthetic construct
US-10-296-085A-26

Query Match
Best Local Similarity 68.7%; Score 879; DB 16; Length 896;
Pred. No. 1.3e-58;
Matches 171; Conservative 25; Mismatches 46; Indels 2; Gaps 1;

QY 1 EVLOQSGPDLVKPGASVKISCKASYFTGYMHVVKSHGKSLIEWIGRINPNNGVTLY 60
Db 516 EVLOQSGPELVKPGASMKISCKASYFTGYTMNVKQSHGKNLEWMGLINPYKGVSTY 575
QY 61 NQKFKDKATLTVDKSSSTAYMELSLTSDSAVYYCARSTMI--TNYVMDYGVSTVTV 118
Db 576 NQKFKDKATLTVDKSSSTAYMELSLTSDSAVYYCARSGYYGDSWDYFDVWGAGTTTV 635
QY 119 SSGGGSGGGTGGGGSSIVMTQTPTFLVLSAGDRVITTCASQSVSNDVAVYQKPGOS 178
Db 636 SSGGGSGGGGGGGSDIQMTQTSSLSASLGDRVTISCRASQDIRNVLNYYQKPDGT 695
QY 179 PTLISYTSRRYAGVDPDRFIGSGYGTDTFTTISTLQAE DLAVYFCQDQVNSPPTFGGK 238
Db 696 VKLLIYTSRLHSGVPSKFSGSGGTDYSLTISNLEQEDIATYFCQDQNTLPWTAGGK 755
QY 239 LEIK 242
Db 756 LEIK 759

RESULT 14
US-10-496-179-2
; Sequence 2, Application US/10496179
; Publication No. US20050033034A1
; GENERAL INFORMATION:
; APPLICANT: Novartis AG
; APPLICANT: Engel, Guenter
; TITLE OF INVENTION: New combination
; FILE REFERENCE: TX/4-32202A
; CURRENT APPLICATION NUMBER: US/10/496,179
; PRIOR FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: GB 0128509.7
; PRIOR FILING DATE: 2001-11-28
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 896
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(896)
; OTHER INFORMATION: synthetic construct
US-10-496-179-2

Query Match
Best Local Similarity 68.7%; Score 879; DB 17; Length 896;
Pred. No. 1.3e-58;
Matches 171; Conservative 25; Mismatches 46; Indels 2; Gaps 1;

QY 1 EVLOQSGPDLVKPGASVKISCKASYFTGYMHVVKSHGKSLIEWIGRINPNNGVTLY 60
Db 516 EVLOQSGPELVKPGASMKISCKASYFTGYTMNVKQSHGKNLEWMGLINPYKGVSTY 575
QY 61 NQKFKDKATLTVDKSSSTAYMELSLTSDSAVYYCARSTMI--TNYVMDYGVSTVTV 118
Db 576 NQKFKDKATLTVDKSSSTAYMELSLTSDSAVYYCARSGYYGDSWDYFDVWGAGTTTV 635
QY 119 SSGGGSGGGTGGGGSSIVMTQTPTFLVLSAGDRVITTCASQSVSNDVAVYQKPGOS 178
Db 636 SSGGGSGGGGGGGSDIQMTQTSSLSASLGDRVTISCRASQDIRNVLNYYQKPDGT 695
QY 179 PTLISYTSRRYAGVDPDRFIGSGYGTDTFTTISTLQAE DLAVYFCQDQVNSPPTFGGK 238
Db 696 VKLLIYTSRLHSGVPSKFSGSGGTDYSLTISNLEQEDIATYFCQDQNTLPWTAGGK 755
QY 239 LEIK 242
Db 756 LEIK 759

Search completed: March 11, 2005, 15:07:46
Job time : 139 secs
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 896
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: synthetic construct
US-10-296-085A-26

Query Match
Best Local Similarity 68.7%; Score 879; DB 16; Length 896;
Pred. No. 1.3e-58;
Matches 171; Conservative 25; Mismatches 46; Indels 2; Gaps 1;

QY 119 SSGGGSGGGTGGGGSSIVMTQTPTFLVLSAGDRVITTCASQSVSNDVAVYQKPGOS 178
Db 636 SSGGGSGGGGGGGSDIQMTQTSSLSASLGDRVTISCRASQDIRNVLNYYQKPDGT 695
QY 179 PTLISYTSRRYAGVDPDRFIGSGYGTDTFTTISTLQAE DLAVYFCQDQVNSPPTFGGK 238
Db 696 VKLLIYTSRLHSGVPSKFSGSGGTDYSLTISNLEQEDIATYFCQDQNTLPWTAGGK 755
QY 239 LEIK 242
Db 756 LEIK 759

RESULT 15
US-10-496-179-3
; Sequence 3, Application US/10496179
; Publication No. US20050033034A1
; GENERAL INFORMATION:
; APPLICANT: Novartis AG
; APPLICANT: Engel, Guenter
; TITLE OF INVENTION: New combination
; FILE REFERENCE: TX/4-32202A
; CURRENT APPLICATION NUMBER: US/10/496,179
; PRIOR FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: GB 0128509.7
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: GB 0128510.5
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 896
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(896)
; OTHER INFORMATION: synthetic construct
US-10-496-179-3

Query Match
Best Local Similarity 70.1%; Score 879; DB 17; Length 896;
Pred. No. 1.3e-58;
Matches 171; Conservative 25; Mismatches 46; Indels 2; Gaps 1;

QY 1 EVLOQSGPDLVKPGASVKISCKASYFTGYMHVVKSHGKSLIEWIGRINPNNGVTLY 60
Db 516 EVLOQSGPELVKPGASMKISCKASYFTGYTMNVKQSHGKNLEWMGLINPYKGVSTY 575
QY 61 NQKFKDKATLTVDKSSSTAYMELSLTSDSAVYYCARSTMI--TNYVMDYGVSTVTV 118
Db 576 NQKFKDKATLTVDKSSSTAYMELSLTSDSAVYYCARSGYYGDSWDYFDVWGAGTTTV 635
QY 119 SSGGGSGGGTGGGGSSIVMTQTPTFLVLSAGDRVITTCASQSVSNDVAVYQKPGOS 178
Db 636 SSGGGSGGGGGGGSDIQMTQTSSLSASLGDRVTISCRASQDIRNVLNYYQKPDGT 695
QY 179 PTLISYTSRRYAGVDPDRFIGSGYGTDTFTTISTLQAE DLAVYFCQDQVNSPPTFGGK 238
Db 696 VKLLIYTSRLHSGVPSKFSGSGGTDYSLTISNLEQEDIATYFCQDQNTLPWTAGGK 755
QY 239 LEIK 242
Db 756 LEIK 759

Search completed: March 11, 2005, 15:07:46
Job time : 139 secs
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OM protein - protein search, using sw model

Run on: March 11, 2005, 14:49:22 ; Search time 16 Seconds
(without alignments)
1461.292 Million cell updates/sec

Title: US-10-016-686-1
Perfect score: 1279
Sequence: 1 EVQLQQSGFDLVKPGASVKI.....QQDYNSPPTFGGKTKLEIKR 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues 283416
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|----------|--------------------|
| 1 | 731.5 | 57.2 | 268 | 2 A56446 | Ig heavy chain V r |
| 2 | 710 | 55.5 | 249 | 2 S41374 | single chain Fv an |
| 3 | 646 | 50.5 | 233 | 2 JCS322 | p53 specific singl |
| 4 | 516 | 40.3 | 120 | 2 A49982 | Ig heavy chain V r |
| 5 | 502 | 39.2 | 128 | 2 I37267 | Ig heavy chain V r |
| 6 | 501 | 39.2 | 135 | 2 PS0057 | Ig heavy chain pre |
| 7 | 498 | 38.9 | 139 | 2 A27609 | Ig heavy chain pre |
| 8 | 496.5 | 38.8 | 225 | 2 S37484 | Ig kappa chain - m |
| 9 | 494 | 38.6 | 128 | 2 C37267 | Ig heavy chain V r |
| 10 | 483.5 | 37.8 | 151 | 2 PL0011 | Ig heavy chain pre |
| 11 | 481.5 | 37.6 | 144 | 2 B30502 | Ig heavy chain V r |
| 12 | 481 | 37.6 | 114 | 2 S26319 | Ig heavy chain V r |
| 13 | 480.5 | 37.6 | 117 | 1 MHMS4E | Ig heavy chain V r |
| 14 | 480.5 | 37.6 | 140 | 2 T01407 | Ig heavy chain (my |
| 15 | 479.5 | 37.5 | 117 | 1 MHMSJ5 | Ig heavy chain V r |
| 16 | 479 | 37.5 | 118 | 1 MHMS38 | Ig heavy chain V r |
| 17 | 478.5 | 37.4 | 125 | 2 PH0100 | Ig heavy chain V r |
| 18 | 478 | 37.4 | 112 | 2 S09957 | Ig heavy chain V-D |
| 19 | 476 | 37.2 | 122 | 2 E37267 | Ig heavy chain V r |
| 20 | 476 | 37.2 | 137 | 2 H32513 | Ig heavy chain pre |
| 21 | 475 | 37.1 | 122 | 2 PH0887 | Ig heavy chain V r |
| 22 | 474 | 37.1 | 119 | 2 F30502 | Ig heavy chain V r |
| 23 | 472 | 36.9 | 128 | 2 A37267 | Ig heavy chain V r |
| 24 | 471.5 | 36.9 | 119 | 2 B53285 | Ig heavy chain V a |
| 25 | 471 | 36.8 | 107 | 2 S26320 | Ig heavy chain V r |
| 26 | 465 | 36.4 | 113 | 2 S55535 | Ig heavy chain V r |
| 27 | 465 | 36.4 | 120 | 2 F45722 | anti-glycoprotein |
| 28 | 465 | 36.4 | 127 | 2 S04577 | Ig kappa chain pre |
| 29 | 464 | 36.3 | 120 | 2 E45722 | anti-glycoprotein |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 463.5 | 36.2 | 121 | 2 F37266 | Ig heavy chain V r |
| 31 | 462 | 36.1 | 139 | 2 PS0024 | Ig heavy chain pre |
| 32 | 461.5 | 36.1 | 113 | 2 PH0974 | Ig heavy chain V r |
| 33 | 461.5 | 36.1 | 119 | 2 PH0099 | Ig heavy chain V r |
| 34 | 460 | 36.0 | 113 | 2 S55534 | Ig heavy chain V r |
| 35 | 459.5 | 35.9 | 125 | 2 S20639 | Ig heavy chain V r |
| 36 | 459.5 | 35.9 | 138 | 2 PH0105 | anti-digoxin trans |
| 37 | 458.5 | 35.8 | 117 | 2 S03305 | Ig heavy chain V r |
| 38 | 458 | 35.8 | 120 | 2 S41394 | Ig heavy chain V r |
| 39 | 457 | 35.7 | 287 | 4 PC4402 | pepB leader/Ig hea |
| 40 | 456 | 35.7 | 150 | 2 PN0444 | Ig heavy chain V r |
| 41 | 456 | 35.7 | 246 | 2 S38950 | Ig gamma chain - m |
| 42 | 456 | 35.7 | 446 | 2 S40295 | Ig gamma-2a chain |
| 43 | 455 | 35.6 | 107 | 2 S09964 | Ig kappa chain V-J |
| 44 | 455 | 35.6 | 108 | 2 PH0975 | Ig heavy chain V r |
| 45 | 453.5 | 35.5 | 118 | 2 PL0200 | anti-DNA autoantib |

ALIGNMENTS

RESULT 1

A56446
IG heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C:Species: Mus musculus (house mouse)
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C:Accession: A56446
R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical to the anti-digoxin antibody
A:Reference number: A56446; MUID:95229583; PMID:7713873
A:Accession: A56446
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-268 <TAN>
A:Cross-references: GB:U20617
C:Keywords: heterotetramer; immunoglobulin

Query Match 57.2%; Score 731.5; DB 2; Length 268;
Best Local Similarity 58.8%; Pred. No. 4e-45;
Matches 143; Conservative 36; Mismatches 61; Indels 3; Gaps 3;

| | | | |
|----|-----|--|-----|
| QY | 1 | EVQLQQSGFDLVKPGASVKISCKASGYSTFGYIMHWKQSHGKSLIEWIGRINPNNGVTLY | 60 |
| DB | 3 | QVKLQSGAELVKPGASVKLSCTTSGFNIKDTYIMHWKQRPQGLEWIGRIAPANGITKY | 62 |
| QY | 61 | NQKFKDKAILTVDKSSTTAYMELRLTSDSDSAVYICARSTMITNYVMDYWGQVTSVTSS | 120 |
| DB | 63 | DKPFGKATIAADTSNTAYLQLSLTSDTNAVYICA-SYLTTRY-ENTWGGQTTVTSS | 120 |
| QY | 121 | GGGSGGGGTGGGSSIVMTQTPTFLVSGADRVITCKASQSVSNVDVAVYQKPGQSPT | 180 |
| DB | 121 | GGGSGGGGSGGGGSDIELTQSPAIMASLGEKVTMSCRASSV-NFIWYQKSDASPK | 179 |
| QY | 181 | LLISVTSRYAGVPRPFTGSGYGTFTTISTLOEDLAVYFCQDYNSPPTFGGKTKLE | 240 |
| DB | 180 | LVVYTTSHLPGPVAPRFGSGSGNSYSLTSSMEGEDATYYCQPTSSPPTFGSGTKLE | 239 |
| QY | 241 | IKR 243 | |
| DB | 240 | IKR 242 | |

RESULT 2

S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv antibody
A:Reference number: S41374

A:Accession: S41374
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: EMBL:Z29480

Query Match 55.5%; Score 710; DB 2; Length 249;
Best Local Similarity 56.6%; Pred. No. 1.3e-43;
Matches 141; Conservative 41; Mismatches 59; Indels 8; Gaps 3;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYMHVWKSHGKSLRWIGRINPNNGVTLY 60
DB 1 QVLOQSGAELVRFPGASVKLSCTASGFNFKDDYIHVWKQRPKEGLEWIAPIAPASGVKY 60

QY 61 NQFKDKAILTVDKSSTTAYMELRLSTSDSAVYYCA-RSTMITNVMDYWGQVTSVTYS 119
DB 61 VRFQDKAVITADTSNTAYLLSLTSDTAVYYCARRDLTYS--LGWGGGSTVTYS 118

QY 120 SGGGSGGGGTGGGGSSIVMTQPTFLVLSAGDRVTITCKASQSV-----SNDVAVYQOK 174
DB 119 SRGGSGGGGGGGGDIELTQPPSVWVLPGESVSISSRSKSLYSDDGSYLFWFLQR 178

QY 175 PGOSPTLLISYTSRVAGVDPDRIGSGYGTDFTTISTLOAEDLAVYFCQDYNSPPTFG 234
DB 179 PGOSPOLLIYRMSNLASGVDPDRFSGSGGTFTLRISRVEADGVYYCQHREYPLTFG 238

QY 235 GGTGLEIKR 243
DB 239 AGTKLEIKR 247

RESULT 3

JC5322
p53 specific single-chain antibody Pab421 - human
C:Species: Homo sapiens (man)
C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: JC5322
R:Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: JC5322; MUID:97168950; PMID:9016757
A:Accession: JC5322
A:Molecule type: mRNA
A:Residues: 1-233 <JAN>
A:Experimental source: hybridoma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 50.5%; Score 646; DB 2; Length 233;
Best Local Similarity 55.2%; Pred. No. 4.2e-39;
Matches 133; Conservative 27; Mismatches 69; Indels 12; Gaps 3;

QY 5 QOSGPDPLVKPGASVKISCKASGYSTGYMHVWKSHGKSLRWIGRINPNNGVTLYNOKF 64
DB 1 QESGAELVRSASGASVKLSCTTSFNFINDYMHVWKRPKEGLEWIGRIDPDENGADMTRSS 60

QY 65 KDAILTVDKSSTTAYMELRLSTSDSAVYYCARSTMITNVMDYWGQVTSVTSSGGGG 124
DB 61 GVKATMTADTSNTAYLQLSLTSDTAVYYC-----NAGMDYWGQGTITVTSSGGGG 113

QY 125 SGGGGTGGGGSSIVMTQPTFLVLSAGDRVTITCKASQSVND-----VAVYQOKPQSPPT 180
DB 114 SGRASGGGGSDIELTQSPASLAVSGQRATISCRASKSVTSYGYSYMHWNOKPQPPR 173

QY 181 LLISYTSRVAGVDPDRIGSGYGTDFTTISTLOAEDLAVYFCQDYNSPPTFGGTTKLE 240
DB 174 LLILVSNLESVGPAPRFSSGGGTDFTLNHPVEEDAATYYCQH-IRELTSEGGTTKLE 232

QY 241 I 241
DB 233 I 233

RESULT 4

A49982

Ig heavy chain V region (BA7.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: A49982
R:Lin, C.; Kleber-Emmons, T.; Vallalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.R.
J. Biol. Chem. 269, 2805-2813, 1994
A:Title: Topology of an aniloride-binding protein.
A:Reference number: A49982; MUID:94132051; PMID:8300613
A:Accession: A49982
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <LIN>
A:Cross-references: GB:L24802; NID:g452096; PIDN:AAA98740.1; PID:g452097
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 40.3%; Score 516; DB 2; Length 120;
Best Local Similarity 82.5%; Pred. No. 3.6e-30;
Matches 99; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYMHVWKSHGKSLRWIGRINPNNGVTLY 60
DB 1 EVLOQSGPELVKPGASVKISCKASGYSTGYIHWKQSHVKSLEWIGHISPYNGATTY 60

QY 61 NQFKDKAILTVDKSSTTAYMELRLSTSDSAVYYCARSTMITNVMDYWGQVTSVTSS 120
DB 61 NONFKDTASLTVDKSSSTAYMELSLTSDSAVYYCARFNYGHYTMGYWGQVTSVTSS 120

RESULT 5

I37267
Ig heavy chain V region (129) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C:Accession: I37267
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; MUID:9117923; PMID:1706720
A:Accession: I37267
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-128 <RUF>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 39.2%; Score 502; DB 2; Length 128;
Best Local Similarity 79.7%; Pred. No. 3.9e-29;
Matches 98; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

QY 2 VLOQSGDPLVKPGASVKISCKASGYSTGYMHVWKSHGKSLRWIGRINPNNGVTLYN 61
DB 6 VLOQSGPELVKPGASVKISCKTSGTYTFTYTHWVQSHGKSLRWIGRINPNNGTSYN 65

QY 62 QKFKDKAILTVDKSSTTAYMELRLSTSDSAVYYCARSTMIT---NYVMDYWGQVTSVT 117
DB 66 QKFKDKAILTVDKSSTAYMELRLSTSDSAVYYCARRGLTTVAKSYFYDWGQGTILT 125

QY 118 VSS 120
DB 126 VSS 128

RESULT 6

PS0057
Ig heavy chain precursor V region (PAR) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
C:Accession: PS0057
R:Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.

J. Biochem. 104, 337-343, 1988
A;Title: Biased expression of variable region gene families of the immunoglobulin heavy
A;Reference number: P50057; MUID:89197817; PMID:2467902
A;Accession: P50057
A;Molecule type: DNA
A;Residues: 1-135 <YAO>
A;Cross-references: GB:D00307; NID:g220448; PIDN:BAR00213.1; PID:g220449
A;Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly
C;Comment: The gene encoding this protein was isolated from a hybridoma that produces an
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-135/Product: Ig heavy chain V region PAR #status predicted <VAR>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 39.2%; Score 501; DB 2; Length 135;
Best Local Similarity 82.5%; Pred. No. 4.8e-29;
Matches 99; Conservative 6; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVLQOQSGPDLVKPGASVKISKASGYSTGYMHVQSHGKSLWIGRINPNNGVTLY 60
DB 20 EVLQOQSGPELVKPGASVKISKASGYSTGYFMNVKQSHGKSLWIGRINPNYNGDTFY 79
QY 61 NQKFKDKATLTVDKSSSTAYMELRSITSDSAVYCARSTMTNTYVMDYWGQVTSVTYSS 120
DB 80 NQKFKGKATLTVDKSSSTAHMELRSITSDSAVYCARSTMTNTYVMDYWGQVTSVTYSS 135

RESULT 7
A27609
Ig heavy chain precursor V region (129) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: A27609
R;Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988
A;Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain switch
A;Reference number: A27609; MUID:88154467; PMID:3126234
A;Accession: A27609
A;Molecule type: DNA
A;Residues: 1-139 <KLE>
A;Cross-references: EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PID:g5533992
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-139/Product: Ig heavy chain V region 129 #status predicted <VAR>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 38.9%; Score 498; DB 2; Length 139;
Best Local Similarity 80.0%; Pred. No. 8.2e-29;
Matches 96; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVLQOQSGPDLVKPGASVKISKASGYSTGYMHVQSHGKSLWIGRINPNNGVTLY 60
DB 20 EVLQOQSGPELVKPGASVKISKASGYSTGYFMNVKQSHGKSLWIGRINPNYNDYTSY 79
QY 61 NQKFKDKATLTVDKSSSTAYMELRSITSDSAVYCARSTMTNTYVMDYWGQVTSVTYSS 120
DB 80 NQKFKGKATLTVDKSSSTAYMQLNSITSDSAVYCARSTMTNTYVMDYWGQVTSVTYSS 139

RESULT 8
S37484
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C;Accession: S37484
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37484

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-225 <DUC>
A;Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 38.8%; Score 496.5; DB 2; Length 225;
Best Local Similarity 87.5%; Pred. No. 1.8e-28;
Matches 98; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 132 GGGSSIVMTQPTLLYSAGDRVTITCKASVSNDAVYQKPGQSPDLLISYTSRYA 191
DB 9 GAHGSIVMTQPTKFLLSAGDRVTITCKASVSNDAVYQKPGQSPDLLISYTSRYT 68
QY 192 GVPDRFIGSGYGTDTFTTISTLOAEDLAVYFCQDYNPPTFGGCTKLEIKR 243
DB 69 GVPDRFTSGYGTDTFTTISTVQAEDLAVYFCQDYSS-YTFGGCTKLEIKR 119

RESULT 9
C37267
Ig heavy chain V region (py69) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C;Accession: C37267
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti-
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: C37267
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-128 <RUF>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 38.6%; Score 494; DB 2; Length 128;
Best Local Similarity 77.2%; Pred. No. 1.4e-28;
Matches 95; Conservative 9; Mismatches 15; Indels 4; Gaps 1;

QY 2 VOLQOQSGPDLVKPGASVKISKASGYSTGYMHVQSHGKSLWIGRINPNNGVTLYN 61
DB 6 VOLQOQSGPELVKPGASVKISKCTGYTFTYTHVQSHGKSLWIGRINPNNGSTYN 65
QY 62 QKFKDKATLTVDKSSSTAYMELRSITSDSAVYCARSTMTNTYVMDYWGQVTSVT 117
DB 66 QKFKGKATLTVDKSSSTAYMELRSITSDSAVYCARRGPYGNYYTSTYFDYWGQVTLT 125

QY 118 VSS 120
DB 126 VSS 128

RESULT 10
PL0011
Ig heavy chain precursor V region (4C11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0011
R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.
A;Reference number: PL0011; MUID:88142863; PMID:3125424
A;Accession: PL0011
A;Molecule type: mRNA
A;Residues: 1-151 <CHS>
A;Experimental source: cell line 4C11
C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcholine
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>


```

F:20-136/Product: Ig heavy chain V region 4C11: #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:50-54/Region: complementarity-determining 1
F:69-85/Region: complementarity-determining 2
F:118-125/Region: complementarity-determining 3
F:137-151/Domain: C region (fragment) #status predicted <COR>

Query Match 37.8%; Score 483.5; DB 2; Length 151;
Best Local Similarity 78.0%; Pred. No. 9.6e-28;
Matches 96; Conservative 7; Mismatches 11; Indels 9; Gaps 2;

Qy 1 EVQLQQSGPDLVKGASVKISCKASGYSTFGYVHWVKQSHGKSLWIGRINPNNGVTLY 60
Db 20 EVQLQQSGPELLKFGASVKISCKASGYTFDDYVHWVKQSHGKSLWIGGDFPNYDNTFY 79

Qy 61 NQKFKDKAILTVDKSSTAYMELRSLTSEDSAVVYCARSTMITNY---VMDYWGQVTSVT 117
Db 80 NEKFKDKATLTVDKSSSTAYMELRSLTSEDSAVVYCA-----SYDYGALDYGQGTSTV 133

Qy 118 VSS 120
Db 134 VSS 136

RESULT 11
B30502
Ig heavy chain V region (D444) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Nov-1998 #sequence_revision 03-Nov-1998 #text_change 21-Jan-2000
C:Accession: B30502
R:Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice
A:Reference number: A30502; MUID:88315787; PMID:2457627
A:Accession: B30502
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-144 <EIL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 37.6%; Score 481.5; DB 2; Length 144;
Best Local Similarity 59.1%; Pred. No. 1.3e-27;
Matches 97; Conservative 16; Mismatches 28; Indels 23; Gaps 2;

Qy 1 EVQLQQSGPDLVKGASVKISCKASGYSTFGYVHWVKQSHGKSLWIGRINPNNGVTLY 60
Db 1 EVQLQQSGPELVKPGASVKMSCKASGYITIGYVHWVKQRPQGGLAWIGYINPDGTTY 60

Qy 61 NQKFKDKAILTVDKSSTAYMELRSLTSEDSAVVYCARSTMITNYMDYWGQVTSVTS 120
Db 61 NEKFKDKATLTSDKSSSTAYTELSSLASEDSAAVYCARGG-----FDYWGQGTTLTV-- 112

Qy 121 GGGGSGGGGTGGGGSSIVMTQTFLLVSAGDRAVTTTCASQSV 164
Db 113 -----DILLQTSFALLSVSPGRVSPFSCRASQSI 141

RESULT 12
S26319
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C:Accession: S26319
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26319
A:Molecule type: mRNA
A:Residues: 1-114 <STA>
A:Cross-references: EMBL:X59172

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Qy 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHWVKQSHGKSLIEWIGRIINPNNGVTLY 60
Db 20 EVLOQSGPELVKPGASVAMSKASGYTFDYIMKWVKQSHGKSLIEWIGDIINPNNGGTSY 79
Qy 61 NQKFKDKAILTVDKSSTAYMELRLSITSDSAVYYCARSTMITNYYMDYWGQVTSVTVSS 120
Db 80 NQKFKGKAILTVDKSSSTAYMQLNSLTSDSAVYYCARDY---YDFVDMGAGTTVTVSS 136

RESULT 15
MHMSJ5
Ig heavy chain V region (J558) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C:Accession: A26242
R:Schilling, J.; Cleavinger, B.; Davie, J.M.; Hood, L.
Nature 283, 35-40, 1980
A:Title: Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements
A:Reference number: A26242; MUID:80078170; PMID:6765983
A:Accession: A26242
A:Molecule type: protein
A:Residues: 1-117 <SCH>
A:Cross-references: UNIPROT:P01757
A:Note: the sequences of 10 hybridoma proteins that also bind dextran differ from that of
C:Comment: This protein binds dextran.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; hybridoma; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
F:22-96/Disulfide bonds: #status predicted

Query Match 37.5%; Score 479.5; DB 1; Length 117;
Best Local Similarity 78.3%; Pred. No. 1.4e-27;
Matches 94; Conservative 7; Mismatches 16; Indels 3; Gaps 1;
Qy 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHWVKQSHGKSLIEWIGRIINPNNGVTLY 60
Db 1 EVLOQSGPELVKPGASVAMSKASGYTFDYIMKWVKQSHGKSLIEWIGDIINPNNGGTSY 60
Qy 61 NQKFKDKAILTVDKSSTAYMELRLSITSDSAVYYCARSTMITNYYMDYWGQVTSVTVSS 120
Db 61 NQKFKGKAILTVDKSSSTAYMQLNSLTSDSAVYYCARDY---YDFVDMGAGTTVTVSS 117

Search completed: March 11, 2005, 14:56:09
Job time : 23 secs

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OM protein - protein search, using sw model

Run on: March 11, 2005, 14:48:42 ; Search time 63 Seconds
(without alignments)
1975.163 Million cell updates/sec

Title: US-10-016-686-1
Perfect score: 1279
Sequence: 1 EVOLQSGPDLVKPGASVKI.....QODYNSPPTFGGKLEIKR 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03: *
1: uniprot_eprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 828.5 | 64.8 | 243 | 2 Q7TQM2 | Q7TQM2 mus musculus |
| 2 | 780.5 | 61.0 | 244 | 2 Q652C8 | Q652C8 homo sapien |
| 3 | 753.5 | 58.9 | 255 | 2 Q6XB05 | Q6XB05 mus musculus |
| 4 | 743.5 | 58.1 | 487 | 2 Q652L2 | Q652L2 mus sp. fv/ |
| 5 | 702 | 54.9 | 298 | 2 Q9QYF0 | Q9QYF0 synthetic c |
| 6 | 701.5 | 54.8 | 241 | 2 Q921A6 | Q921A6 mus musculus |
| 7 | 698.5 | 54.6 | 240 | 2 Q652C9 | Q652C9 homo sapien |
| 8 | 655 | 51.2 | 248 | 2 Q652Q7 | Q652Q7 mus sp. b3(|
| 9 | 577 | 45.1 | 218 | 2 Q925S1 | Q925S1 mus musculus |
| 10 | 507.5 | 39.7 | 117 | 2 Q9QXE9 | Q9QXE9 mus musculus |
| 11 | 501.5 | 39.2 | 170 | 2 Q925S2 | Q925S2 mus musculus |
| 12 | 499 | 39.0 | 470 | 2 Q7TKK1 | Q7TKK1 mus musculus |
| 13 | 497.5 | 38.9 | 117 | 2 Q9QXF0 | Q9QXF0 mus musculus |
| 14 | 491.5 | 38.4 | 134 | 2 Q652R6 | Q652R6 mus musculus |
| 15 | 491 | 38.4 | 472 | 2 Q6P7A7 | Q6P7A7 mus musculus |
| 16 | 484 | 37.8 | 145 | 2 Q924Q9 | Q924Q9 mus musculus |
| 17 | 483 | 37.8 | 145 | 2 Q924Q6 | Q924Q6 mus musculus |
| 18 | 480.5 | 37.6 | 117 | 1 HV12_MOUSE | P01756 mus musculus |
| 19 | 479.5 | 37.5 | 117 | 1 HV13_MOUSE | P01757 mus musculus |
| 20 | 479 | 37.5 | 118 | 1 HV51_MOUSE | P06330 mus musculus |
| 21 | 476 | 37.2 | 145 | 2 Q924R4 | Q924R4 mus musculus |
| 22 | 468 | 36.6 | 99 | 2 Q9JL74 | Q9JL74 mus musculus |
| 23 | 468 | 36.6 | 145 | 2 Q924R1 | Q924R1 mus musculus |
| 24 | 467.5 | 36.6 | 146 | 2 Q924Q3 | Q924Q3 mus musculus |
| 25 | 465.5 | 36.4 | 488 | 2 Q91WR1 | Q91WR1 mus musculus |
| 26 | 464.5 | 36.3 | 123 | 2 Q8VIJ1 | Q8VIJ1 mus musculus |
| 27 | 464 | 36.3 | 145 | 2 Q924P7 | Q924P7 mus musculus |
| 28 | 463 | 36.2 | 143 | 2 Q924R0 | Q924R0 mus musculus |
| 29 | 456.5 | 35.7 | 142 | 2 Q924Q1 | Q924Q1 mus musculus |
| 30 | 456 | 35.7 | 143 | 2 Q924P6 | Q924P6 mus musculus |
| 31 | 455.5 | 35.6 | 140 | 2 Q924R2 | Q924R2 mus musculus |

ALIGNMENTS

RESULT 1

Q7TQM2 PRELIMINARY; PRT; 243 AA.

AC Q7TQM2; DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DE 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE SCFV 6H8 protein (Fragment).
GN Name=SCFV 6H8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/C;
RX MEDLINE=28853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
RA Peter J.C., Eftekhari P., Billiald P., Wallukat G., Hoebeke J.;
RT "scfv single chain antibody variable fragment as inverse agonist for
RT the beta-2 adrenergic receptor."
RL J. Biol. Chem. 278:36740-36747(2003).
DR EMBL; AJ574851; CAE00495.1; -.
DR HSSP; P01751; 1A6W.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON_TER
SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DC4F76 CRC64;

Query Match. 64.8%; Score 828.5; DB 2; Length 243;
Best Local Similarity 66.1%; Pred. No. 4.1e-58;
Matches 160; Conservative 30; Mismatches 47; Indels 5; Gaps 2;

QY 1 EVOLQSGPDLVKPGASVKISCKASGYSTGYMHVVKQSHKSLIEWIGRINPNNGVTLY 60
DB 1 QVOLQSGSELVRPGASVKLSCKASGYTFTTYMHVVKQRHQGLEWIGNIYFGSGITNY 60
QY 61 NOKPKDKAILTVDKSSTTAYMELRLSTSDSAVYVCARSTMTITNYVMDYVGQVTSVTSS 120
DB 61 DEKFNKGILTVDRSSSTAYMHLSSLASDSAVYVCARG----GRGLDWAGAGTILTVSS 116
QY 121 GGGSGGGGTGGGSSIVMTQTPTFLVYAGDRVITCKASQSVSNDAVYQOQFGQSP 180
DB 117 GGGSGGGSGGGGSDIQMTQSSSFSVSLGDRVITCKASDIYNRLAWYQOQFGNAPR 176
QY 181 LLISVTSRYAGVDRPFGSGYDTFTTISTLOEDLAVYFCQDYNSPPTFGGKLE 240
DB 177 LLISGATLETGVPGRFSGSGKDYTLISLTQEDVATYVCOQ-YWSTRTFGGGKLE 235
QY 241 IK 242
DB 236 IK 237

Q924r8 mus musculus
Q8k0f2 mus musculus
Q8k172 mus musculus
P01751 mus musculus
Q924q7 mus musculus
Q924r3 mus musculus
Q924q8 mus musculus
Q924r6 mus musculus
Q920e8 mus musculus
Q924q4 mus musculus
Q924p8 mus musculus
Q924r7 mus musculus
Q9d8l4 mus musculus
Q6pjb2 mus musculus


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DR PROSITE; PS00290; IG_MHC; UNKNOWN 1;
SQ SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;

Query Match
Best Local Similarity 58.1%; Score 743.5; DB 2; Length 487;
Matches 144; Conservative 37; Mismatches 54; Indels 7; Gaps 2;

QY 1 EVLOQSGPDLVKPGASVKISKASGYSTGYMHVVKSHGKSLWIGRIINPNNGVTLY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVLOQSDAELVKPGASVKISKASGYSTGYMHVVKSHGKSLWIGRIINPNNGVTLY 79
QY 61 NQKFKDKAILTVDKSSTTAYMELRSITSDSAVYICARSTMTITNYVMDYVGQVTSVTSS 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 NEKFKGKATLADKSSSTAYMQLNSLTSDSAVYFCRS-----YVGHGQGTTLT-GS 132
QY 121 GGGSGGGGTGGGGSSIVMTQTPTFLVLSAGDRVTITCKASQSVSNDAVYQKPKQSPT 180
Db 133 GGGSGGGGTGGGGSSIVMTQTPTFLVLSAGDRVTITCKASQSVSNDAVYQKPKQSPT 192
QY 181 LLISVTSRYAGVDPDRFIGSGYGTDTFTTISTLQAEADLAVYFCQDYNBPPTFGGKTLE 240
Db 193 LLVYAATNLADGVPSRFSFGSGGTQYSLKINSIQSDFDGSGYTCQHFWTPTTFFGGKTLE 252
QY 241 IK 242
Db :|||
253 IK 254

RESULT 5
Q9QYF0 PRELIMINARY; PRT; 298 AA.
ID Q9QYF0
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CN 8 single chain antibody.
GN Name-CN 8 scFv;
OS synthetic construct.
OC other sequences; artificial sequences.
OX NCBI_TaxID=32630;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=20183931; PubMed=10706631; DOI=10.1073/pnas.050589197;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phage display subtraction
RT method.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590 (2000).
DR EMBL; AB036341; BAA88633.1; -.
DR PIR; A33933; A33933.
DR PIR; S19112; S19112.
DR HSSP; P01820; 1A70.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match
Best Local Similarity 54.9%; Score 702; DB 2; Length 298;
Matches 132; Conservative 41; Mismatches 68; Indels 2; Gaps 1;

QY 1 EVLOQSGPDLVKPGASVKISKASGYSTGYMHVVKSHGKSLWIGRIINPNNGVTLY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
40 QVLOQSGGLVKPGSLKSLCAASGDSFRVMSVWRQAPKGLWIGIINPDASTIN 99
QY 61 NQKFKDKAILTVDKSSTTAYMELRSITSDSAVYICARSTMTITNYVMDYVGQVTSVTSS 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
100 TPLSKDKFIISRDNAKNTLYLQMSKVRSEDALYICARASYGHSA--YVGHGQGTTLT 157
QY 121 GGGSGGGGTGGGGSSIVMTQTPTFLVLSAGDRVTITCKASQSVSNDAVYQKPKQSPT 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
158 GGGSGGGGTGGGGSSIVMTQTPTFLVLSAGDRVTITCKASQSVSNDAVYQKPKQSPT 217
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QY 181 LLISVTSRYAGVDPDRFIGSGYGTDTFTTISTLQAEADLAVYFCQDYNBPPTFGGKTLE 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
218 LLVYNAKTILADGVPSRFSFGSGGTQYSLKINSIQSDFDGSGYTCQHFWTPTTFFGGKTLE 277
QY 241 IKR 243
Db :|||
278 IKR 280

RESULT 6
Q921A6 PRELIMINARY; PRT; 241 AA.
ID Q921A6
AC Q921A6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819 (1997).
DR EMBL; U88067; AAB48044.1; -.
DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSSP; P01607; 1BWW.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1_1
FT NON_TER 241 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match
Best Local Similarity 54.8%; Score 701.5; DB 2; Length 241;
Matches 133; Conservative 47; Mismatches 58; Indels 7; Gaps 4;

QY 1 EVLOQSGPDLVKPGASVKISKASGYSTGYMHVVKSHGKSLWIGRIINPNNGVTLY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 QVLOQSGPELKKPGETVKISKASGYTPTDYGMNVKQAPGKGLKMMGWINTYTGEPT 60
QY 61 NQKFKDKAILTVDKSSTTAYMELRSITSDSAVYICARSTMTITNYVMDYVGQVTSVTSS 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 ADDFKGRFAFSLTASATLQINLNKEDTATYFCARGLDRYF--DWGQGTTLTSS 118
QY 121 GGGSGGGGTGGGGSSIVMTQTPTFLVLSAGDRVTITCKASQSVSNDAVYQKPKQSPT 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
119 GGGSGGGGTGGGGSSIVMTQTPTFLVLSAGDRVTITCKASQSVSNDAVYQKPKGPR 178
QY 181 LLISVTSRY--AGVDPDRFIGSGYGTDTFTTISTLQAEADLAVYFCQDYNBPPTFGGKT 238
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
179 --SAHTLHIYIQGIPSRFSFGSGRDSYFSISNLEPEDIATYICLH-YDNLHTFGGKT 235
QY 239 LEIKR 243
Db :|||
236 LEIKR 240

RESULT 7
Q65ZC9 PRELIMINARY; PRT; 240 AA.
ID Q65ZC9
AC Q65ZC9;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
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DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC STRAIN=C1g/7;
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 1
FT NON_TER 240 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 54.6%; Score 698.5; DB 2; Length 240;
Best Local Similarity 56.0%; Pred. No. 9.2e-48;
Matches 136; Conservative 36; Mismatches 68; Indels 3; Gaps 1;

QY 1 EVQLQQSGPDLVKPGASVKISCKASGYSTGYMHVKQSHGKSLIEWIGRINPNNGVTLY 60
DB 1 QVQLVQSGGLVQPQGLSLRLSCAAGFTFSYGMHWVRQAPGKGLEWVAIVSYDSNKYY 60

QY 61 NQKFKDKAILTVDKSSTTAYMELRLSTSEDSAVYYCARSTMTITNYVMDYWGQVTSVTYSS 120
DB 61 ADSVKGRTISRDNKNTLYLQWNSLRADTAIVYCARD---WGDSLDPWKGKGLTVTVSS 117

QY 121 GGGSGGGGTGGGSSIVMTQTPTFLVYSGDRVTITCKASQSVNDVAVYQKQSPPT 180
DB 118 GGGSGGGGTGGGSDIQMTQSPFLSLASIGDRVTITCRASEGIYRWLAWYQKQPKAPK 177

QY 181 LIISVTSRYAGVPRDFIGSGYGTDTFTTISLQAEEDLAVYFCQDQYNSPPTFGG 240
DB 178 LIYKASSLASRAPERFSGSGGTDTFTLTISSLPQDPATYICQYNSYPLTFGGG 237

QY 241 IKR 243
DB 238 IKR 240

RESULT 8
Q65Z07 PRELIMINARY; PRT; 248 AA.
AC Q65Z07;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE B3(Fv)-PE40 (Fragment).
DE Name=B3(Fv)-PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]_TaxID=10095;
RP SEQUENCE FROM N.A.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;
RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete
RT regression of a human carcinoma in mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
DR EMBL; S57990; AAB19971.2; -.

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DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 248 248
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 51.2%; Score 655; DB 2; Length 248;
Best Local Similarity 51.8%; Pred. No. 2.8e-44;
Matches 128; Conservative 45; Mismatches 68; Indels 6; Gaps 3;

QY 1 EVQLQQSGPDLVKPGASVKISCKASGYSTGYMHVKQSHGKSLIEWIGRINPNNGVTLY 60
DB 2 DVKLVEGGGLVQPQGLSLRLSCAAGFTFSYGMHWVRQAPGKGLEWVAIVSYDSNKYY 61

QY 61 NQKFKDKAILTVDKSSTTAYMELRLSTSEDSAVYYCARSTMTITNYVMDYWGQVTSVTYSS 120
DB 62 SDTVKGRFTISRDNARNTLYLQWNSLRKSEDTAIVYSCARG-LAWGAWFAFYWGQGLTVTVSS 120

QY 121 GGGSGGGGTGGGSSIVMTQTPTFLVYSGDRVTITCKASQSV--SND---VAVYQKQKP 175
DB 121 GGGSGGGGTGGGSDVLTQSPFLSLVSLGDAQISCRSQIIVHSGNTLYLEWYLOKP 180

QY 176 GQSPTLILSYTSRYAGVPRDFIGSGYGTDTFTTISTLQAEEDLAVYFCQDQYNSPPTFGG 235
DB 181 GQSPKLLLYKVNRFSGVPRDFSGSGGTDTFTLISRVEADLGVYFCQSHVPTFTGS 240

QY 236 GTKLEIK 242
DB 241 GTKLEIK 247

RESULT 9
Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR HSSP; P01665; 1QNZ.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 218 218
SQ SEQUENCE 218 AA; 527E4FA8F7982817 CRC64;

Query Match 45.1%; Score 577; DB 2; Length 218;
Best Local Similarity 51.4%; Pred. No. 4e-38;

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RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055910; AAH55910.1; -
DR HSSP; P01865; 1KB5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51727 MW; 6D90E4DF896BB090 CRC64;

Query Match 39.0%; Score 499; DB 2; Length 470;
Best Local Similarity 63.4%; Pred. No. 1.6e-31;
Matches 104; Conservative 11; Mismatches 27; Indels 22; Gaps 3;

QY 1 EVQLQSGPDLVKPGASVKISKASGYFTGYMHVWKSHGKSLGWIGRINPNNGVTLY 60
DB 20 EVQLQSGPELVKPGASVKISKASGYFTGYMHVWKSHGKSLGWIGLVNPNNGDTSY 79
QY 61 NQKFKDKAILTVDKSSSTAYMELSLTSDSAVYICARSTMTINY-VMDYWGQVTSVTVS 119
DB 80 NQKFKGKATLVDKSSSTAYMELSLTSDSAVYICARYYSGSYWYFDVWGAGTITVVS 139
QY 120 SGGGGSGGGGTGGGGSIWVTPTEFLV-----SAGDRVITTC 158
DB 140 SA-----TTTAPSVYPLVPGCGDTSGSSVTLCG 167

RESULT 13

Q9QXF0 PRELIMINARY; PRT; 117 AA.
AC Q9QXF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TREMBLrel. 26, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch B.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; A0225171; CAB65236.1; -
DR PIR; PH0973; PH0973.
DR HSSP; P01751; INOB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 38.9%; Score 497.5; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 4.3e-32;
Matches 96; Conservative 8; Mismatches 13; Indels 3; Gaps 1;

QY 1 EVQLQSGPDLVKPGASVKISKASGYFTGYMHVWKSHGKSLGWIGRINPNNGVTLY 60
DB 1 EVQLQSGPELVKPGASVKMSCKASGYFTDYMKWKVQSPKSLGWIGDINPNNGTST 60
QY 61 NQKFKDKAILTVDKSSSTAYMELSLTSDSAVYICARSTMTINYMDYWGQVTSVTVS 120

DB 61 NQKFKGKATLVDKSSSTAYMQLNSLTSDSAVYICARD---KDYFDYWGQGITLTVSS 117
RESULT 14
Q65ZR6 PRELIMINARY; PRT; 134 AA.
AC Q65ZR6;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Ab 126.33 heavy chain variable and joining regions (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91237115; PubMed=1709665;
RA Rueff-Juy D., Marche P.N., Drapier A.-M., Cazenave P.-A.;
RT "Junctional diversity of H and L chains allows the coexpression of two mutually exclusive idiotopes (Id1104 and Id1558).";
RL J. Immunol. 146:4024-4030 (1991).
DR EMBL; M74139; AAA37776.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 134 AA; 14908 MW; 1852D86D26FC7567 CRC64;

Query Match 38.4%; Score 491.5; DB 2; Length 134;
Best Local Similarity 80.0%; Pred. No. 1.5e-31;
Matches 96; Conservative 8; Mismatches 13; Indels 3; Gaps 1;

QY 1 EVQLQSGPDLVKPGASVKISKASGYFTGYMHVWKSHGKSLGWIGRINPNNGVTLY 60
DB 18 EVQLQSGPELVKPGASVKMSCKASGYFTDYMKWKVQSPKSLGWIGDINPNNGTST 77
QY 61 NQKFKDKAILTVDKSSSTAYMELSLTSDSAVYICARSTMTINYMDYWGQVTSVTVS 120
DB 78 NQKFKGKATLVDKSSSTAYMQLNSLTSDSAVYICARD---YSYFDYWGQGITLTVSS 134

RESULT 15

Q6PJA7 PRELIMINARY; PRT; 472 AA.
AC Q6PJA7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018535; AAH18535.1; --
DR HSSP; P01865; 1K85.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_
SQ SEQUENCE 472 AA; 52299 MW; 165169C23D55D4AB CRC64;

Query Match 38.4%; Score 491; DB 2; Length 472;
Best Local Similarity 51.1%; Pred. No. 7e-31;
Matches 112; Conservative 20; Mismatches 49; Indels 38; Gaps 5;
QY 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHWVKSHGKSLGWIGRINPNNGVTLY 60
DB 20 EVQLQSGPELVKPGASVKMSKASGYTFSDYIMHWVKSHGKSLGWIGYIYPNNGNGY 79
QY 61 NQKFKDKATLTVDKSTTAYMELRLTSDSAVYYCAR---STMTITNYMDYMGQVTSVT 117
DB 80 NQKFKGKATLTVDKSSSTAYMELRLTSDSAVYYCARGYISYYSDHYDFYWGQGTIT 139
QY 118 VSSG-----CGSGGGGGTGG-----GGSSIVMTQTPTFLVLS 149
DB 140 VSSAKTAPSVYPLAPVCGDTTGGSVTLGCLVKGVPPBPVTLTWNSSLSGVTFFPAVL 199
QY 150 AGDRVITCKASQSVNDVAWYQQKPGQSPFTLLISYTS 188
DB 200 QSDLYTLSSSVTVTS---TW----PSQITCNVAHPAS 231

Search completed: March 11, 2005, 14:55:45
Job time : 68 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 14:58:51 ; Search time 3609 Seconds
(without alignments)
9787.712 Million cell updates/sec

Title: US-10-016-686-5
Perfect score: 729
Sequence: 1 gaggtccagcttcagcagtc.....ccaagctggaatacaacgg 729

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_ste.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 728.2 | 99.9 | 729 | 6 | BD136150 Vector. 9 |
| 2 | 728.2 | 99.9 | 729 | 6 | AX002778 Sequence |
| 3 | 728.2 | 99.9 | 729 | 6 | AX149544 Sequence |
| 4 | 727.4 | 99.8 | 729 | 6 | BD136268 Enhanceme |
| 5 | 727.4 | 99.8 | 729 | 6 | AX018532 Sequence |
| 6 | 727.4 | 99.8 | 729 | 6 | AX018608 Sequence |
| 7 | 727.4 | 99.8 | 1807 | 6 | BD136151 Vector. 9 |
| 8 | 724.4 | 99.8 | 1807 | 6 | AX002779 Sequence |
| 9 | 724.4 | 99.4 | 1467 | 6 | BD136152 Vector. 9 |
| 10 | 724.4 | 99.4 | 1467 | 6 | AX002780 Sequence |
| 11 | 724.4 | 99.4 | 1467 | 6 | AX149546 Sequence |
| 12 | 724.2 | 99.3 | 1518 | 6 | BD136154 Vector. 9 |
| 13 | 724.2 | 99.3 | 1518 | 6 | AX002782 Sequence |
| 14 | 724.2 | 99.3 | 1518 | 6 | AX149550 Sequence |
| 15 | 721 | 98.9 | 1796 | 6 | AX149547 Sequence |
| 16 | 721 | 98.9 | 2090 | 6 | BD136155 Vector. 9 |
| 17 | 721 | 98.9 | 2090 | 6 | AX002783 Sequence |
| 18 | 721 | 98.9 | 2090 | 6 | AX149551 Sequence |
| 19 | 481.2 | 66.0 | 10511 | 6 | AX666316 Sequence |

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| 20 | 463.6 | 63.6 | 804 | 6 | CQ868387 | CQ868387 Sequence |
| 21 | 462 | 63.4 | 723 | 12 | AF332008 | AF332008 Synthetic |
| 22 | 458.2 | 62.9 | 756 | 6 | A76868 | A76868 Sequence 6 |
| 23 | 458.2 | 62.9 | 756 | 6 | AR456298 | AR456298 Sequence |
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| 25 | 450.8 | 61.8 | 735 | 12 | AF162710 | AF162710 Synthetic |
| 26 | 442 | 60.6 | 1725 | 6 | AX001509 | AX001509 Sequence |
| 27 | 441.2 | 60.5 | 735 | 12 | SC0250760 | AJ250760 Mus muscu |
| 28 | 440.6 | 60.4 | 753 | 12 | SC0416563 | AJ416563 Synthetic |
| 29 | 439.4 | 60.3 | 1701 | 12 | SC0564232 | AJ564232 Synthetic |
| 30 | 438.8 | 60.2 | 864 | 6 | AR3227 | AR3227 Sequence 47 |
| 31 | 438.8 | 60.2 | 864 | 6 | AR182952 | AR182952 Sequence |
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| 33 | 438.8 | 60.2 | 2019 | 6 | AR3211 | AR3211 Sequence 31 |
| 34 | 438.8 | 60.2 | 2019 | 6 | AR182939 | AR182939 Sequence |
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| 36 | 438.8 | 60.2 | 2025 | 6 | AR3217 | AR3217 Sequence 37 |
| 37 | 438.8 | 60.2 | 2025 | 6 | AR182944 | AR182944 Sequence |
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| 39 | 438.6 | 60.2 | 1668 | 6 | AX001511 | AX001511 Sequence |
| 40 | 438.6 | 60.2 | 2438 | 6 | CQ812173 | CQ812173 Sequence |
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| 42 | 437.8 | 60.1 | 726 | 6 | AX100174 | AX100174 Sequence |
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| 44 | 432.8 | 59.4 | 810 | 6 | CQ832138 | CQ832138 Sequence |
| 45 | 432.8 | 59.4 | 810 | 6 | CQ832288 | CQ832288 Sequence |

ALIGNMENTS

RESULT 1
BD136150
LOCUS BD136150 729 bp DNA linear PAT 18-SEP-2002
DEFINITION Vector.
ACCESSION BD136150
VERSION BD136150.1 GI:23231095
KEYWORDS JP 2002507117-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 729)
AUTHORS other sequences; artificial sequences.
Kingsman,S.M., Bebbington,C.R., Ellard,F.M., Carroll,M.W. and Myers,K.A.
TITLE Vector
JOURNAL Patent: JP 2002507117-A 1 05-MAR-2002;
OXFORD BIOMEDICA LTD
COMMENT OS Artificial Sequence
PN JP 2002507117-A/1
PD 05-MAR-2002
PF 04-JUN-1998 JP 1999501858
PR 04-JUN-1997 GB 9711579.4,20-JUN-1997 GB 9713150.2 PR
04-JUL-1997 GB 9714230.1
PI SUSAN MARY KINGSMAN,CHRISTOPHER ROBERT BEBBINGTON,FIONA PI
MARGARET ELLARD,
PI MILES WILLIAM CARROLL,KEVIN ALAN MYERS
PC C12N15/85,A61K48/00
CC Description of Artificial Sequence: DNA
FH Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.7e-219;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GAGGTCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 60
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LOCUS AX002778 729 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from Patent WO9855607.
ACCESSION AX002778
VERSION AX002778.1 GI:9885103
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Bebbington,C.R., Carroll,M.W., Ellard,F.M., Kingsman,S.M. and Myers,K.A.
TITLE Vector
JOURNAL Patent: WO 9855607-A 1 10-DEC-1998;
BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
ELLARD FIONA MARGARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN
ALAN (GB); OXFORD BIOMEDICA LTD (GB)
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ORIGIN

Query Match 99.9%; Score 728.2; DB 6; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.7e-219;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGTCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 60
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Db 721 ATCAAACGG 729

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| LOCUS | BD136268 | | |
| DEFINITION | Enhancement of prodrug activation. | | |
| ACCESSION | BD136268 | | |
| VERSION | BD136268.1 | GI:23231213 | |
| KEYWORDS | JP 2002505341-A/21. | | |
| SOURCE | synthetic construct | | |
| ORGANISM | synthetic construct | | |
| REFERENCE | 1 (bases 1 to 729) | | |
| AUTHORS | Stratford,I.J., Patterson,A.V., Kingsman,S.M., Kan,O., Griffiths,I.L. and Mitrophanous,K. | | |
| TITLE | Enhancement of prodrug activation | | |
| JOURNAL | Patent: JP 2002505341-A 21 19-FEB-2002; | | |
| COMMENT | OXFORD BIOMEDICA LTD | | |
| | OS Artificial Sequence | | |
| | PN JP 2002505341-A/21 | | |
| | PD 19-FEB-2002 | | |
| | PF 05-MAR-1999 JP 2000534657 | | |
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| | PR 29-JAN-1999 GB 9902081.0 | | |
| | PI IAN JAMES STRATFORD,ADAM VORN PATTERSON,SUSAN MARY KINGSMAN,ON | | |
| | PI KAN, | | |
| | PI LEIGH GRIFFITHS,KYRIACOS MITROPHANOUS | | |
| | PC A61K47/48,A61K35/76,A61K38/44,A61K45/00,A61K48/00,A61P9/10,PC | | |
| | A61P29/00, | | |
| | PC A61P35/00,A61P43/00,C12N5/10,C12N7/00,C12N9/02,C12N15/09,PC | | |
| | A61K37/50, | | |
| | PC C12N5/00,C12N15/00 | | |
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| | | Indels 0; | Gaps 0; |
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| Db | 61 | TCTGCAAGGCTTCGTGTTACTCATTCACATGGCTACTACATGCATCGGTGAAGCAGCAGC | 120 |
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| Db | 241 | ATGGAGCTCCGACGCTGACATCTGAGGACTCTGGGCTCTATTACTGTGCAAGATCTACT | 300 |
| Qy | 301 | ATGATTACGAATCTATGTTATGACTACTGGGCTCAAGTAACTCAGTCAACGCTCTCTCA | 360 |
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| Qy | 361 | GGTGGTGGGAGCGGTGGTGGGCACTTGGCGGCGGATCTAGTATTGTGATGACC | 420 |
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| Qy | 481 | AGTCAGAGTGTGAGTAATGATGTGGTACCAACAGAGCAGGCTGCAAGCTGCTCTACA | 540 |
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| Qy | 661 | TATTTCTGTGCAAGATTAATAATCTCTCCGACGTTCCGCTGGGAGGCCACCAAGCTGGAA | 720 |
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| VERSION | BD136151.1 GI:23231096 |
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| SOURCE | synthetic construct |
| ORGANISM | other sequences; artificial sequences. |
| REFERENCE | 1 (bases 1 to 1807) |
| AUTHORS | Kingsman,S.M., Bebbington,C.R., Ellard,F.M., Carroll,M.W. and Myers,K.A. |
| TITLE | Vector |
| JOURNAL | Patent: JP 2002507117-A 2 05-MAR-2002; |
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| | PN JP 2002507117-A/2 |
| | PD 05-MAR-2002 |
| | PF 04-JUN-1998 JP 1999501858 |
| | PR 04-JUN-1997 GB 9711579.4, 20-JUN-1997 GB 9713150.2 PR |
| | 04-JUL-1997 GB 9714230.1 |

| | |
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| PI | SUSAN MARY KINGSMAN, CHRISTOPHER ROBERT BEBBINGTON, FIONA PI |
| MARGARET ELLARD, | |
| PI | MILES WILLIAM CARROLL, KEVIN ALAN MYERS |
| PC | C12N15/85,A61K48/00 |
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| Db | 129 TCCTGCAAGGCTTCTGTTTACTCAITTCACCTGGCTACTACATGACCTGGGTGAAGCAGAGC 188 |
| Qy | 121 CATGGAAGAGCCTTGAGTGGATTGACGTATTAATCTTAACAAATGGTGTACTCTCTAC 180 |
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| Qy | 301 ATGATTACGAATCTATGTTATGACTACTGGGCTCAAGTAACTCAGTCAACGCTCTCTCA 360 |
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 DEFINITION Sequence 2 from Patent WO9855607.
 ACCESSION AX002779
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 KEYWORDS synthetic construct
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 AUTHORS Bebbington, C.R., Carroll, M.W., Ellard, F.M., Kingsman, S.M. and Myers, K.A.
 TITLE Vector
 JOURNAL Patent: WO 9855607-A 2 10-DEC-1998;
 BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
 ELLARD FTONA MARGARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN
 ALAN (GB); OXFORD BIOMEDICA LTD (GB)
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ORIGIN

| | Query Match | 99.8%; | Score 727.4; | DB 6; | Length 1807; |
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| QY | 61 | TCCTGCAAGCTTCTCGTTACTCATTCACTGGCTACTACATGCATCGGGTGAAGCAGAGC | 120 | | |
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| QY | 181 | AACCAGAAATTCGAAGCAAGGCCATATTAATCTGTAGACAAAGTCATCCACACAGCCTAC | 240 | | |
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| AUTHORS | | | | | | |
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| JOURNAL | | | | | | |
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ACCESSION AX149547
VERSION AX149547.1 GI:14347986
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OTHER SEQUENCES; artificial sequences.
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AUTHORS Kingsman,A.O.; Kingsman,S.M.; Bebbington,C.R., Carroll,M.W.,
Ellard,F.M. and Myers,K.A.
TITLE Antibodies
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Oxford Biomedica (UK) Limited (GB)
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ORIGIN

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GenCore version 5.1.6
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SUMMARIES

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| 39 | 416.8 | 57.2 | 891 | 13 | ADS20751 | ADS20751 SBP tagge |
| 40 | 415 | 56.9 | 876 | 4 | AAF30734 | AAF30734 DNA encod |
| 41 | 415 | 56.9 | 969 | 4 | AAF30730 | AAF30730 Antibody |
| 42 | 415 | 56.9 | 2190 | 4 | AAF30729 | AAF30729 Antibody |
| 43 | 413.4 | 56.7 | 716 | 10 | ADC79233 | ADC79233 VK-8-1.9 |
| 44 | 413 | 56.7 | 1920 | 10 | ADH34695 | ADH34695 CE7-speci |
| 45 | 413 | 56.7 | 6834 | 10 | ADH34699 | ADH34699 CE7-speci |

ALIGNMENTS

RESULT 1
AAV80290
ID AAV80290 standard; cDNA; 729 BP.
XX
AC AAV80290;
XX
DT 15-MAR-1999 (first entry)
XX
DE Murine anti-5T4 antigen monoclonal antibody scFv DNA.
XX
KW Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW monoclonal antibody; single chain antibody; scFv; mouse; 5T4scFv.1; ss.
XX
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
PN WO9855607-A2.
XX
PD 10-DEC-1998.
XX
PF 04-JUN-1998; 98WO-GB001627.
XX
PR 04-JUN-1997; 97GB-00011579.
PR 20-JUN-1997; 97GB-00013150.
PR 04-JUL-1997; 97GB-00014230.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
XX
XX WPI; 1999-059910/05.
DR P-PSDB; AAV86002.
XX
XX New vector encoding a tumour interacting protein for treating cancer -
PT contains a desired nucleotide sequence and/or protein which recognises
PT tumours, and is used as a gene delivery system to treat cancer.
XX
PS Example 1; Fig 1A; 82pp; English.
XX
CC This DNA sequence encodes a 5T4 scFv, designated 5T4scFv.1 (see
CC AAV86002), comprising the heavy chain variable region (VH) from the
CC murine 5T4 monoclonal antibody followed by a 15-amino acid flexible

CC linker and the light chain variable region (VL) of the mouse 5T4
CC antibody. The trophoblast cell surface antigen defined by monoclonal
CC antibody 5T4 is expressed at high levels on the cells of a wide variety
CC of human tumours. The 5T4scFv.1 DNA sequence can be used to construct
CC single-chain antibodies (see AAV80291) and scFv fusion constructs (see
CC AAV80292-96). The invention relates to a vector comprising a nucleotide
CC sequence coding for a tumour interacting protein (TIP) and optionally a
CC nucleotide sequence of interest (NOI) which encodes a protein of interest
CC (POI), the vector being capable of delivering the NOI and/or POI to the
CC tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The
CC vector is used to treat cancer, and may also be used as a gene delivery
CC system for introducing at least 1 gene encoding a TIP (preferably a
CC tumour binding protein) into a haematopoietic cell lineage
XX
SQ Sequence 729 BP; 180 A; 178 C; 189 G; 181 T; 0 U; 1 Other;
Query Match 99.9%; Score 728.2; DB 2; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.1e-197;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 60
DB 1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 60
QY 61 TCTGCAAGGCTTCGTGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
DB 61 TCTGCAAGGCTTCGTGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
QY 121 CATGGAAGAGGCTTGAGTGAATGGAAGTATTAATCTTAATCTTAACAAATGGTGTACTCTCTAC 180
DB 121 CATGGAAGAGGCTTGAGTGAATGGAAGTATTAATCTTAATCTTAACAAATGGTGTACTCTCTAC 180
QY 181 AACCGAATTAACGACAGAGCCATTAATTAATCTGAGCAAGTCTATCCACACAGCCTAC 240
DB 181 AACCGAATTAACGACAGAGCCATTAATTAATCTGAGCAAGTCTATCCACACAGCCTAC 240
QY 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
DB 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
QY 301 ATGATTACGAACTATGTTATGAGCTACTGGGGTCAAGTAACTCAGTCAACCGTCTCTCA 360
DB 301 ATGATTACGAACTATGTTATGAGCTACTGGGGTCAAGTAACTCAGTCAACCGTCTCTCA 360
QY 361 GTGGTGGTGGAGCGGTGCGGCACTGCGGCGGATCTAGTATTGTGATGACC 420
DB 361 GTGGTGGTGGAGCGGTGCGGCACTGCGGCGGATCTAGTATTGTGATGACC 420
QY 421 CAGACTCCACATTCCTGCTTTTTCAGCAGAGACAGGGTTACCATACCTGCAAGGCC 480
DB 421 CAGACTCCACATTCCTGCTTTTTCAGCAGAGACAGGGTTACCATACCTGCAAGGCC 480
QY 481 AGTCAGAGTGTGAGTAATGATAGTGTGGTACCAACAGAGCCAGGGCAGTCTCTCA 540
DB 481 AGTCAGAGTGTGAGTAATGATAGTGTGGTACCAACAGAGCCAGGGCAGTCTCTCA 540
QY 541 CTGCTCATATCTATACATCCAGTCTGCTAGCTGAGTCCCTGATCGCTTCATTGGCAGT 600
DB 541 CTGCTCATATCTATACATCCAGTCTGCTAGCTGAGTCCCTGATCGCTTCATTGGCAGT 600
QY 601 GGATATGGACGGATTTCACTTTTCACTATCAGCATCAGCATTTTTCAGGCTGAAGACCTGGCAGTT 660
DB 601 GGATATGGACGGATTTCACTTTTCACTATCAGCATCAGCATTTTTCAGGCTGAAGACCTGGCAGTT 660
QY 661 TATTTCTGTGACAGATTAATTAATTTCTCTCGACGTTCTGGTGGAGGACCAAGCTGGAA 720
DB 661 TATTTCTGTGACAGATTAATTAATTTCTCTCGACGTTCTGGTGGAGGACCAAGCTGGAA 720
QY 721 ATCAACGG 729
DB 721 ATCAACGG 729

RESULT 2
AAF89729
XX AAF89729 standard; DNA; 729 BP.
AC AAF89729;
XX
DT 23-JUL-2001 (first entry)
DE Nucleotide sequence of a 5T4 scFv designated 5T4ScFv.1.
XX
KW Single chain antibody; scFv; inflammatory disease; arthritis; cancer;
KW hypersensitivity; autoimmune disease; central nervous system disorder;
KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW Helicobacter-related disease; immune disorder; ss.
XX
OS Synthetic.
OS Mus sp.
XX
XX Location/Qualifiers
FT CDS
FT 1..729
FT /*tag= a
FT /transl_except= (pos: 505..507, aa: Ala)
XX
PN WO200136486-A2.
XX
PD 25-MAY-2001.
XX
PF 13-NOV-2000; 200WO-GB004317.
XX
PR 18-NOV-1999; 99WO-GB003859.
PR 15-FEB-2000; 2000GB-00003527.
PR 02-MAR-2000; 2000GB-00005071.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingman A, Kingman SM, Bebbington CR, Carroll MW, Ellard FM;
PI Myers KA;
XX
DR WPI: 2001-343805/36.
DR P-PSDB; AAB83835.
XX
PT Use of single chain antibody capable of recognizing a disease associated
PT molecule for manufacturing a medicament for preventing and/or treating a
PT disease condition associated with disease associated molecule.
XX
PS Claim 7; Fig 1; 118pp; English.
XX
CC The specification describes the use of a single chain antibody (scFv),
CC which is capable of recognizing a disease associated molecule in the
CC manufacture of a medicament for the prevention and treatment of a disease
CC condition. The scFv antibody is useful in the manufacture of a
CC medicament, for affecting a disease in vivo, for preparing a
CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC treatment of a disease. The scFv antibody is also useful for treating
CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC disease, cancers, central nervous system disorders including Parkinson's
CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC related diseases, and other immune disorders. The present sequence
CC encodes a 5T4 scFv of the invention. The antibody comprises the VH and VL
CC regions from murine 5T4 monoclonal antibody, joined by a linker sequence
XX
SQ Sequence 729 BP; 180 A; 178 C; 189 G; 181 T; 0 U; 1 Other;
Query Match 99.9%; Score 728.2; DB 4; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.1e-197;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 60
DB 1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 60

361 GGTGGTGGAGCGGTGGTGGCGGCACTGGCGGGCGGCTAGTATTGTGATGACC 420
|||
361 GGTGGTGGAGCGGTGGTGGCGGCACTGGCGGGCGGCTAGTATTGTGATGACC 420
|||
421 CAGACTCCCACTCTCTGCTTTGTTGAGGAGAGAGAGGTTACCATTAACCTGCAAGGCC 480
|||
421 CAGACTCCCACTCTCTGCTTTGTTGAGGAGAGAGAGGTTACCATTAACCTGCAAGGCC 480
|||
481 AGTCAGAGTGTAGTATGATGATGTTGTTACCAAGAGCCAGGCGAGTCTCTTACA 540
|||
481 AGTCAGAGTGTAGTATGATGATGTTGTTACCAAGAGCCAGGCGAGTCTCTTACA 540
|||
541 CTGCTCATATPCCATATACATCCAGTCGCTAGCTGGAGTCCCTGATCGCTTCAITGGCAGT 600
|||
541 CTGCTCATATPCCATATACATCCAGTCGCTAGCTGGAGTCCCTGATCGCTTCAITGGCAGT 600
|||
601 GGATATGGAGCGGATTTCACTTTCACATCAGCAGTCTTGAGGCTGAAGACCTGGCAGTT 660
|||
601 GGATATGGAGCGGATTTCACTTTCACATCAGCAGTCTTGAGGCTGAAGACCTGGCAGTT 660
|||
661 TATTTCTGTGAGCAAGATTATATATTTCTCTCCGACGTTGGTGGAGGCGCAGCTGGAA 720
|||
661 TATTTCTGTGAGCAAGATTATATATTTCTCTCCGACGTTGGTGGAGGCGCAGCTGGAA 720
|||
721 ATCAAAACGG 729
|||
721 ATCAAAACGG 729
|||

RESULT 4
AAZ07810
ID AAZ07810 standard; DNA; 729 BP.
XX
AC AAZ07810;
XX
DT 23-NOV-1999 (first entry)
XX
DE 5T4 scFv antibody encoding DNA.
XX
KW Prodrug; localization domain; tumor-selective antibody; cytochrome P450;
KW Prodrug activating domain; modified hematopoietic stem cell; MHSC; tumor;
KW inflammation; atherosclerosis; muscular dystrophy; cerebral malaria;
KW rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; tumor antigen;
KW 5T4 scFv; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 1..729 /*tag= a
FT
XX W09945126-A2.
XX
PN 10-SEP-1999.
XX
PF 05-MAR-1999; 99NO-GB000672.
XX
PR 06-MAR-1998; 98GB-00004841.
PR 19-AUG-1998; 98GB-00018103.
PR 29-JAN-1999; 98GB-00002081.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
XX Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;
PI Mitrophanous K;
XX
DR WPI; 1999-540852/45.
DR P-PSDB; AAY27407.
XX
PT New prodrug activating agent targeted to selected cells or tissues,
PT particularly hypoxic cells, for treating e.g. tumors or inflammation.
XX
PS Example 9; Fig 3F; 149pp; English.

XX
CC The invention provides a new prodrug activating agent that comprises: (i)
CC a localization domain (LD; other than a tumor-selective antibody) and a
CC prodrug activating domain (PAD); (ii) at least one nucleic acid encoding
CC a cytochrome P450 and under control of at least one constitutive or
CC inducible expression control sequence or (iii) a modified hematopoietic
CC stem cell (MHSC) containing at least one nucleic acid encoding a PAD and
CC under control of elements as in (ii). The prodrug activating agent or
CC vectors that express them, are specifically used to treat tumors,
CC inflammation, atherosclerosis and muscular dystrophy, but may also be
CC used to treat many other conditions, e.g. cerebral malaria, rheumatoid
CC arthritis, or conditions associated with hypoxia, hypoglycemia or
CC ischemia, or to deliver antibiotics, antiviral agents, analgesics,
CC anesthetics, anti-inflammatories, antineoplastic agents and diagnostic
CC agents. LD optimize activity of PAD, e.g. by delivering it to selected
CC locations or by delivering it to neighboring cells (bystander effect),
CC and allow a reduction in dose of prodrug, and thus of systemic side-
CC effects. Nucleic acids encoding the agent may be expressed selectively in
CC hypoxic cells. The present sequence represents the DNA encoding the
CC single chain variable antibody fragment against the tumor antigen 5T4
CC (5T4 scFv). 5T4 scFv is used in the construction of a fusion protein
CC comprising 5T4 scFv and a human P450 reductase derivative alP45OR
XX
SQ Sequence 729 BP; 180 A; 179 C; 189 G; 181 T; 0 U; 0 Other;
Query Match 99.8%; Score 727.4; DB 2; Length 729;
Best Local Similarity 99.9%; Pred No. 3.6e-197;
Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAGGTCCAGCTTTCAGCAGTCTGGACCTGACCTGGTGAAGCCCTGGGGCTTCAGTGAAGATA 60
DB 1 GAGGTCCAGCTTTCAGCAGTCTGGACCTGACCTGGTGAAGCCCTGGGGCTTCAGTGAAGATA 60
QY 61 TCCTGCAAGGCTTCGCTTACTTCACTGCTGCTACTATGCTGCTGGTGAAGCAGCAGC 120
DB 61 TCCTGCAAGGCTTCGCTTACTTCACTGCTGCTACTATGCTGCTGGTGAAGCAGCAGC 120
QY 121 CATGGAAGAGCCTTGAGTGGATTGGAGCTTAACTTAATCTTAACTGGTGTACTCTCTAC 180
DB 121 CATGGAAGAGCCTTGAGTGGATTGGAGCTTAACTTAATCTTAACTGGTGTACTCTCTAC 180
QY 181 AACCAAGAAATTCAGGAGCAAGGCCATATAAATCTGAGCAAGATCATCCACACAGCCTAC 240
DB 181 AACCAAGAAATTCAGGAGCAAGGCCATATAAATCTGAGCAAGATCATCCACACAGCCTAC 240
QY 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGCTCAAGTAACTCAGTCACTCTCTCA 300
DB 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGCTCAAGTAACTCAGTCACTCTCTCA 300
QY 301 ATGATTACGAACCTATGTTATGGACTACTGGGCTCAAGTAACTCAGTCACTCTCTCA 360
DB 301 ATGATTACGAACCTATGTTATGGACTACTGGGCTCAAGTAACTCAGTCACTCTCTCA 360
QY 361 GGTGGTGGAGCGGTGGTGGGCGCACTGGCGCGCGCGGATCTAGTATTGTGATGACC 420
DB 361 GGTGGTGGAGCGGTGGTGGGCGCACTGGCGCGCGCGGATCTAGTATTGTGATGACC 420
QY 421 CAGACTCCCACTCTCTGCTTTGTTGAGGAGAGAGAGGTTACCATTAACCTGCAAGGCC 480
DB 421 CAGACTCCCACTCTCTGCTTTGTTGAGGAGAGAGAGGTTACCATTAACCTGCAAGGCC 480
QY 481 AGTCAGAGTGTAGTATGATGATGTTGTTACCAAGAGCCAGGCGAGTCTCTTACA 540
DB 481 AGTCAGAGTGTAGTATGATGATGTTGTTACCAAGAGCCAGGCGAGTCTCTTACA 540
QY 541 CTGCTCATATPCCATATACATCCAGTCGCTAGCTGGAGTCCCTGATCGCTTCAITGGCAGT 600
DB 541 CTGCTCATATPCCATATACATCCAGTCGCTAGCTGGAGTCCCTGATCGCTTCAITGGCAGT 600
QY 601 GGATATGGAGCGGATTTCACTTTCACATCAGCAGTCTTGAGGCTGAAGACCTGGCAGTT 660
DB 601 GGATATGGAGCGGATTTCACTTTCACATCAGCAGTCTTGAGGCTGAAGACCTGGCAGTT 660

QY 661 TATTTCTGTGACAGATTATTAATTTCTCTCCGAGCTTGGTGAGGACCAAGCTGGAA 720
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 661 TATTTCTGTGACAGATTATTAATTTCTCTCCGAGCTTGGTGAGGACCAAGCTGGAA 720
 QY 721 ATCAAAACGG 729
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 721 ATCAAAACGG 729

RESULT 5

AAV80291

ID AAV80291 standard; cDNA; 1807 BP.

XX AC AAV80291;

XX DT 15-MAR-1999 (first entry)

XX DE Anti-5T4 single chain antibody 5T4Sabl DNA.

XX KW Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
 KW monoclonal antibody; single chain antibody; mouse; human; 5T4Sabl; ss.
 XX OS Mus sp.
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.

| Key | Location/Qualifiers |
|--------|--|
| FT CDS | 3..1790 |
| FT | /*tag= a |
| FT | |
| PN | W09855607-A2. |
| XX | |
| PD | 10-DEC-1998. |
| XX | |
| PF | 04-JUN-1998; 98WO-GB001627. |
| XX | |
| PR | 04-JUN-1997; 97GB-00011579. |
| PR | 20-JUN-1997; 97GB-00013150. |
| PR | 04-JUL-1997; 97GB-00014230. |
| XX | |
| PA | (OXFO-) OXFORD BIOMEDICA UK LTD. |
| XX | |
| PI | Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA; |
| XX | |
| DR | WPI: 1999-059910/05. |
| DR | P-PSDB; AAW86003. |
| XX | |

New vector encoding a tumour interacting protein for treating cancer - contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat cancer.

Example 1; Fig 1B; 82pp; English.

This DNA sequence encodes a single chain antibody (Sabl), termed 5T4Sabl (see AAW86003), comprising an scFv derived from murine monoclonal antibody 5T4 (see AAW86002) and the human g1 constant region. It was constructed from cassettes comprising a translation initiation signal and signal peptide (see AAV80297), the sequence of the secreted portion of 5T4scFv.1, and the sequence of the human g1 constant region genomic clone. The trophoblast cell surface antigen defined by 5T4 is expressed at high levels on the cells of a wide variety of human tumours. The invention relates to a vector comprising a nucleotide sequence coding for a tumour interacting protein (TIP) and optionally a nucleotide sequence of interest (NOI) which encodes a protein of interest (POI), the vector being capable of delivering the NOI and/or POI to the tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The vector is used to treat cancer, and may also be used as a gene delivery system for introducing at least 1 gene encoding a TIP (preferably a tumour binding protein) into a haematopoietic cell lineage

Sequence 1807 BP; 432 A; 543 C; 469 G; 363 T; 0 U; 0 Other;

| Query Match | 99.8% | Score 727.4; | DB 2; | Length 1807; |
|---------------------------|---|---------------------|--------|--------------|
| Best Local Similarity | 99.9% | Pred. No. 4.9e-197; | | |
| Matches 728; Conservative | 0; | Mismatches 1; | Indels | Gaps 0; |
| QY 1 | GAGGTCCAGCTTTCAGCAGTCTGGACCTGACCTGGTGAAGCCCTGGGCTTTCAGTGAAGATA | 60 | | |
| Db | | | | |
| QY 69 | GAGGTCCAGCTTTCAGCAGTCTGGACCTGACCTGGTGAAGCCCTGGGCTTTCAGTGAAGATA | 128 | | |
| Db | | | | |
| QY 61 | TCCTGCAAGGCTTCTGGTTACTCAATTCATCTGGCTACTACATGCACTGGGTGAAGCAGAGC | 120 | | |
| Db | | | | |
| QY 129 | TCCTGCAAGGCTTCTGGTTACTCAATTCATCTGGCTACTACATGCACTGGGTGAAGCAGAGC | 188 | | |
| Db | | | | |
| QY 121 | CATGGAAGAGCCTTGAGTGGATTGGAGCTATTAATCTTAACAATGGTGTACTCTCTAC | 180 | | |
| Db | | | | |
| QY 189 | CATGGAAGAGCCTTGAGTGGATTGGAGCTATTAATCTTAACAATGGTGTACTCTCTAC | 248 | | |
| Db | | | | |
| QY 181 | AACAGAAATTCAGGACCAAGGCCATATTAATCTGTAGACAAGTCAATCAACACAGCCTAC | 240 | | |
| Db | | | | |
| QY 249 | AACAGAAATTCAGGACCAAGGCCATATTAATCTGTAGACAAGTCAATCAACACAGCCTAC | 308 | | |
| Db | | | | |
| QY 241 | ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGTCTATTACTGTGCAAGATCTACT | 300 | | |
| Db | | | | |
| QY 309 | ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGTCTATTACTGTGCAAGATCTACT | 368 | | |
| Db | | | | |
| QY 301 | ATGATTACGAATCTGTTATGGACTACTGGGTCAAGTAACTCAGTCAACCTCTCTCA | 360 | | |
| Db | | | | |
| QY 369 | ATGATTACGAATCTGTTATGGACTACTGGGTCAAGTAACTCAGTCAACCTCTCTCA | 428 | | |
| Db | | | | |
| QY 361 | GGTGTGGTGGAGCGGTGGTGGCGGCACCTGGCGCGGATCTAGTATTGTGATGACC | 420 | | |
| Db | | | | |
| QY 429 | GGTGTGGTGGAGCGGTGGTGGCGGCACCTGGCGCGGATCTAGTATTGTGATGACC | 488 | | |
| Db | | | | |
| QY 421 | CAGACTCCACATTCCTCTGTTTTCAGCAGGAGACAGGGTTTACCATACTGCAAGGCC | 480 | | |
| Db | | | | |
| QY 489 | CAGACTCCACATTCCTCTGTTTTCAGCAGGAGACAGGGTTTACCATACTGCAAGGCC | 548 | | |
| Db | | | | |
| QY 481 | AGTCAGAGTGTGAGTAATGATGTAGTTGGTACCAACAGAGCCAGGGCAGTCTCTACA | 540 | | |
| Db | | | | |
| QY 549 | AGTCAGAGTGTGAGTAATGATGTAGTTGGTACCAACAGAGCCAGGGCAGTCTCTACA | 608 | | |
| Db | | | | |
| QY 541 | CTGCTCATATCTATACATCCAGTCGCTACGCTGAGTCCCTGATCGCTTCATTGGCAGT | 600 | | |
| Db | | | | |
| QY 609 | CTGCTCATATCTATACATCCAGTCGCTACGCTGAGTCCCTGATCGCTTCATTGGCAGT | 668 | | |
| Db | | | | |
| QY 601 | GGATATGGAGCGGATTTTCACTTTTCCATCAGCCTTTTGCAGGCTGAAGACCTGGCAGTT | 660 | | |
| Db | | | | |
| QY 669 | GGATATGGAGCGGATTTTCACTTTTCCATCAGCCTTTTGCAGGCTGAAGACCTGGCAGTT | 728 | | |
| Db | | | | |
| QY 661 | TATTTCTGTGCAAGATTATTAATTTCTCTCCGAGCTTGGTGAGGACCAAGCTGGAA | 720 | | |
| Db | | | | |
| QY 729 | TATTTCTGTGCAAGATTATTAATTTCTCTCCGAGCTTGGTGAGGACCAAGCTGGAA | 788 | | |
| Db | | | | |
| QY 721 | ATCAAAACGG 729 | | | |
| Db | | | | |
| QY 789 | ATCAAAACGG 797 | | | |
| Db | | | | |
| RESULT 6 | | | | |
| AAV80292 | | | | |
| ID | AAV80292 standard; cDNA; 1467 BP. | | | |
| XX | AC AAV80292; | | | |
| XX | DT 15-MAR-1999 (first entry) | | | |
| XX | DE Human B7-1.5T4.1 gene fusion, specific for human 5T4. | | | |
| XX | KW Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen; | | | |
| XX | KW monoclonal antibody; single chain antibody; scFv; mouse; human; B7-1; | | | |
| XX | KW co-stimulatory molecule; ss. | | | |
| XX | Mus sp. | | | |
| OS | Homo sapiens. | | | |

PT disease condition associated with disease associated molecule.

PS Claim 8; Fig 2; 118pp; English.

XX The specification describes the use of a single chain antibody (scFv),
CC which is capable of recognizing a disease associated molecule in the
CC manufacture of a medicament for the prevention and treatment of a disease
CC condition. The scFv antibody is useful in the manufacture of a
CC pharmaceutical composition, for in vivo imaging and/or for preparing a
CC treatment of a disease. The scFv antibody is also useful for treating
CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC diseases, cancers, central nervous system disorders including Parkinson's
CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC related diseases, and other immune disorders. The present sequence
CC encodes a B7-1.574.1 fusion protein. This comprises the N-terminus of the
CC 574 scFv is fused after amino acid 215 of human B7-1

XX Sequence 1467 BP; 394 A; 349 C; 352 G; 372 T; 0 U; 0 Other;

Query Match 99.4%; Score 724.4; DB 4; Length 1467;
Best Local Similarity 99.9%; Pred. No. 3.3e-196;
Matches 725; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGTCACGCTTCAGCAGCTGAGACCTGAGCTGGTGAACCTGGGGCTTCAGTGAAGATA 60
DB 739 GAGGTCACGCTTCAGCAGCTGAGACCTGAGCTGGTGAACCTGGGGCTTCAGTGAAGATA 798
QY 61 TCCTGCAAGCTTCGTTACTCATCTGCTGCTACTACATGCTGGGTGAAGCAGG 120
DB 799 TCCTGCAAGCTTCGTTACTCATCTGCTGCTACTACATGCTGGGTGAAGCAGG 858
QY 121 CATGGAAGAGCTTCAGTGGATTGAGCTGATTAATCTTAACCTGATGTTACTCTCTAC 180
DB 859 CATGGAAGAGCTTCAGTGGATTGAGCTGATTAATCTTAACCTGATGTTACTCTCTAC 918
QY 181 AACCCAGAAATTCAGGACAGGCGCATATTAACCTGTAGACAGTCAATCCACAGCCTAC 240
DB 919 AACCCAGAAATTCAGGACAGGCGCATATTAACCTGTAGACAGTCAATCCACAGCCTAC 978
QY 241 ATGGAGCTCGGAGCTGACATCTGAGGACTCTGGGCTTATTACTGTGCAAGATCTACT 300
DB 979 ATGGAGCTCGGAGCTGACATCTGAGGACTCTGGGCTTATTACTGTGCAAGATCTACT 1038
QY 301 ATGATTACCAACTATGTTATGCACTACTGGGGTCAAGTAACTCAGTCAACCGTCTCTCA 360
DB 1039 ATGATTACCAACTATGTTATGCACTACTGGGGTCAAGTAACTCAGTCAACCGTCTCTCA 1098
QY 361 GGTGGTGGTGGAGCGGTGGTGGCGCACTGGCGGCGGATCTAGTATTGTGATGACC 420
DB 1099 GGTGGTGGTGGAGCGGTGGTGGCGCACTGGCGGCGGATCTAGTATTGTGATGACC 1158
QY 421 CAGACTCCACATCTCTGCTGTTTTCAGAGAGACAGGTTACCATACCTGCAAGGCC 480
DB 1159 CAGACTCCACATCTCTGCTGTTTTCAGAGAGACAGGTTACCATACCTGCAAGGCC 1218
QY 481 AGTCAGAGTGTAGTAACTGATGTAGTGTGTGTACCAAGACAGGCGAGTCTCTCTACA 540
DB 1219 AGTCAGAGTGTAGTAACTGATGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1278
QY 541 CTGCTCATATCTCATATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 1279 CTGCTCATATCTCATATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1338
QY 601 GGATATGGAGCGGATTTCTCTTTCACCATCAGACACTTTGAGGCTGAAGCTGGCAGTT 660
DB 1339 GGATATGGAGCGGATTTCTCTTTCACCATCAGACACTTTGAGGCTGAAGCTGGCAGTT 1398
QY 661 TATTTCTGTCAGCAAGATTATATCTCTCTCGACGTTCTGGTGGAGGCCACCAAGCTGGAA 720
DB 1399 TATTTCTGTCAGCAAGATTATATCTCTCTCGACGTTCTGGTGGAGGCCACCAAGCTGGAA 1458

QY 721 ATCAAA 726
DB 1459 ATCAAA 1464

RESULT 8

ID AAV80294 standard; cDNA; 1518 BP.

XX AAV80294;

XX 17-OCT-2003 (revised)

DT 15-MAR-1999 (first entry)

DE B7-1/scFv specific for use in cancer gene therapy.

XX Tumour interacting protein; cancer; gene therapy; vector; 574 antigen;

KW monoclonal antibody; single chain antibody; scFv; mouse; B7-1;

KW co-stimulatory molecule; ss.

OS Mus sp.

OS Chimeric.

XX WO9855607-A2.

XX 10-DEC-1998.

XX 04-JUN-1998; 98WO-GB001627.

PR 04-JUN-1997; 97GB-00011579.

PR 20-JUN-1997; 97GB-00013150.

PR 04-JUL-1997; 97GB-00014230.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

PI Kingman SM, Bebbington CR, Ellard PM, Carroll MW, Myers KA;

XX WPI; 1999-059910/05.

PT New vector encoding a tumour interacting protein for treating cancer -
PT contains a desired nucleotide sequence and/or protein which recognises
PT tumours, and is used as a gene delivery system to treat cancer.

PS Example 10; Page 63-64; 82pp; English.

XX This DNA sequence encodes a fusion protein comprising the extracellular
CC domain of mouse co-stimulatory molecule B7-1 joined via a flexible
CC peptide linker to an scFv (see AAV86002) derived from murine 5T4
CC monoclonal antibody. The fusion can be used to construct a recombinant
CC vector, e.g. retrovirus, lentivirus, adenovirus, poxvirus, vaccinia virus
CC or baculovirus, used for direct treatment of tumour patients. The
CC trophoblast cell surface antigen defined by 5T4 is expressed at high
CC levels on the cells of a wide variety of human tumours. The invention
CC relates to a vector comprising a nucleotide sequence coding for a tumour
CC interacting protein (TIP) and optionally a nucleotide sequence of
CC interest (NOI) which encodes a protein of interest (POI), the vector
CC being capable of delivering the NOI and/or POI to the tumour recognised
CC by the TIP. Delivery can be in vivo or ex vivo. The vector is used to
CC treat cancer, and may also be used as a gene delivery system for introducing
CC at least 1 gene encoding a TIP (preferably a tumour binding protein) into
CC a haematopoietic cell lineage. B7-1 binds specifically to CD28 and CTLA-4
CC present on human CD4 and CD8 cells. (Updated on 17-OCT-2003 to
CC standardise OS field)

XX Sequence 1518 BP; 398 A; 364 C; 371 G; 385 T; 0 U; 0 Other;

Query Match 99.3%; Score 724.2; DB 2; Length 1518;
Best Local Similarity 99.6%; Pred. No. 3.8e-196;
Matches 726; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGGTCACGCTTCAGCAGCTGAGCTGGACCTGAGCTGGTGAACCTGGGGCTTCAGTGAAGATA 60
DB 787 GAGGTCACGCTTCAGCAGCTGAGCTGGACCTGAGCTGGTGAACCTGGGGCTTCAGTGAAGATA 846

| | | | |
|----|------|---|------|
| QY | 61 | TCTGTGAAGGCTTCTGGTTACTCATTTACCTGGCTACTATATGCACTGGGTGAAGCAGAGC | 120 |
| DB | 847 | TCTGTGAAGGCTTCTGGTTACTCATTTACCTGGCTACTATATGCACTGGGTGAAGCAGAGC | 906 |
| QY | 121 | CATGTGAAGAGCCTTGAGTGGATTTGAACGCTATTAATCCCTAACCAATGGTGTACTCTCTAC | 180 |
| DB | 907 | CATGTGAAGAGCCTTGAGTGGATTTGAACGCTATTAATCCCTAACCAATGGTGTACTCTCTAC | 966 |
| QY | 181 | AACACAGAAATTCAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACACACAGCCTAC | 240 |
| DB | 967 | AACACAGAAATTCAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACACAGCCTAC | 1026 |
| QY | 241 | ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGCGGCTTATTACTGTGCAAGATCTTACT | 300 |
| DB | 1027 | ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGCGGCTTATTACTGTGCAAGATCTTACT | 1086 |
| QY | 301 | ATGATTTACGAACATATGTTATGGACTACTGGGTCAGTAACCTCAGTCACCGCTCTCCTCA | 360 |
| DB | 1087 | ATGATTTACGAACATATGTTATGGACTACTGGGTCAGTAACCTCAGTCACCGCTCTCCTCA | 1146 |
| QY | 361 | GGTGGTGGTGGGAGCGGTGTTGGCGGCACATGGCGGGCGGATCTAGTATTTGTGATGACC | 420 |
| DB | 1147 | GGTGGTGGTGGGAGCGGTGTTGGCGGCACATGGCGGGCGGATCTAGTATTTGTGATGACC | 1206 |
| QY | 421 | CAGACTCCACATTTCTGCTTGTTCAGCAGGAGACAGGGTTACCATTAACCTGCAAGGCC | 480 |
| DB | 1207 | CAGACTCCACATTTCTGCTTGTTCAGCAGGAGACAGGGTTACCATTAACCTGCAAGGCC | 1266 |
| QY | 481 | AGTCAGAGTGTGAGTAATGATGTAGDTTGGTATCCACACAGAAGCCAGGGCAGTCTCCTACA | 540 |
| DB | 1267 | AGTCAGAGTGTGAGTAATGATGTAGDTTGGTATCCACACAGAAGCCAGGGCAGTCTCCTACA | 1326 |
| QY | 541 | CTGCTCATATCTTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTTGGCAGT | 600 |
| DB | 1327 | CTGCTCATATCTTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTTGGCAGT | 1386 |
| QY | 601 | GGATATGGGACGATTTCACTTTCCACATCAGACATTTGACAGCTGAGACCTGGCAGTT | 660 |
| DB | 1387 | GGATATGGGACGATTTCACTTTCCACATCAGACATTTGACAGCTGAGACCTGGCAGTT | 1446 |
| QY | 661 | TATTTTCTGTGAGCAAGATTATAATTTCTCTCCGACGTTTCGGTGGAGGCACCAAGCTGGAA | 720 |
| DB | 1447 | TATTTTCTGTGAGCAAGATTATAATTTCTCTCCGACGTTTCGGTGGAGGCACCAAGCTGGAA | 1506 |
| QY | 721 | ATCAAAACGG | 729 |
| DB | 1507 | ATCAAAACGG | 1515 |

RESULT 9

AAAF89732

AAF89732
ID AAF89732 standard; DNA: 1518 BP.

XX
XX
25160 JMY DT

AC AAF89732;

DT 23-JUL-2001 (first entry)

XXXXXXXXXXXX

DE Nucleotide sequence of a B7 link ScFv sequence.

XX Single chain antibody; SCFv; inflammatory disease; arthritis; cancer;
KW hypersensitivity; autoimmune disease; central nervous system disorder;
KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW Helicobacter-related disease; immune disorder; ss.

XX NS Synthetic

OS
synthetic.
Homo sapiens.

XX
или варить.

PN WO200136486-A2.

XX

PD 25-MAY-2001.

XX

| | |
|-----------------------|---|
| PF | 13-NOV-2000; 2000WO-GB004317. |
| XX | |
| PR | 18-NOV-1999; 99WO-GB003859. |
| PR | 15-FEB-2000; 2000GB-00003527. |
| PR | 02-MAR-2000; 2000GB-00005071. |
| XX | |
| XX | (OXFO-) OXFORD BIOMEDICA UK LTD. |
| PA | |
| XX | Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FW, Myers KA; |
| PI | |
| PI | WPI; 2001-343805/36. |
| DR | |
| XX | |
| PT | Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule. |
| PT | |
| XX | |
| XX | Example 8; Fig 5; 119pp; English. |
| XX | |
| CC | The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's disease, periodontal diseases, cardiopulmonary diseases, cardiovascular diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-related diseases, and other immune disorders. The present sequence encodes a B7 link ScFv sequence. A human B7 sequence is linked to a ScFv of the invention |
| CC | |
| XX | |
| XX | Sequence 1518 BP; 398 A; 364 C; 371 G; 385 T; 0 U; 0 Other; |
| XX | |
| Query Match | 99.3%; Score 724.2; DB 4; Length 1518; |
| Best Local Similarity | 99.6%; Pred. No. 3.8e-196; |
| Matches | 726; Conservative 0; Mismatches 3; Indels 0; Gaps 0; |
| QY | 1 GAGGTCACGCTTCGAGCTCGGACCTGACCTGCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60 |
| DB | 787 GAGGTCACGCTTCGAGCTCGGACCTGACCTGCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846 |
| QY | 61 TCTCTCAAGGCTTCTGGTTACTCATTCACCTGGCTACTACATGCACCTGGGTGAAGCAGAGC 120 |
| DB | 847 TCTCTCAAGGCTTCTGGTTACTCATTCACCTGGCTACTACATGCACCTGGGTGAAGCAGAGC 906 |
| QY | 121 CATGGAAGAGGCTTCGAGTGGATTGGAAGCTATTAAATCCTAACAAATGGTGTACTCTCTAC 180 |
| DB | 907 CATGGAAGAGGCTTCGAGTGGATTGGAAGCTATTAAATCCTAACAAATGGTGTACTCTCTAC 966 |
| QY | 181 AACCCAGAAATTCAGGAAGAAGGCATATTAACTGTAGACAAGTCAATCCACAGCGCTAC 240 |
| DB | 967 AACCCAGAAATTCAGGAAGAAGGCATATTAACTGTAGACAAGTCAATCCACAGCGCTAC 1026 |
| QY | 241 ATGGAGCTCGGAGCGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTTACT 300 |
| DB | 1027 ATGGAGCTCGGAGCGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTTACT 1086 |
| QY | 301 ATGATTACGAACCTATGTTATGGACTACTGGGCTCAAGTAAACCTCAGTCACCGTCTCCTCA 360 |
| DB | 1087 ATGATTACGAACCTATGTTATGGACTACTGGGCTCAAGTAAACCTCAGTCACCGTCTCCTCA 1146 |
| QY | 361 GGTGTGTGGGAGCGGTGGTGGCGGCATCTGGCGGCGGCGGATCTAGTATTGTGATGACC 420 |
| DB | 1147 GGTGTGTGGGAGCGGTGGTGGCGGCATCTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206 |
| QY | 421 CAGACTCCACATTCCTGCTGTTTTCAGCAGAGAGCAGGTTTACCATTAACCTTCAAGGCC 480 |
| DB | 1207 CAGACTCCACATTCCTGCTGTTTTCAGCAGAGAGCAGGTTTACCATTAACCTTCAAGGCC 1266 |
| QY | 481 AGTCAGAGTGTGAGTAATGATGTAGTDTGGTATCCAAACAGAAGCCAGGCGAGTCTCCTACA 540 |

Db 1267 AGTCAGAGTGTAGTAAATGATGATGCTTGTGTACCAACAGAGCCAGGGCAGTCTCTACA 1326
 Qy 541 CTGCTCATATCCTATACATCCAGTCTAGCTAGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
 Db 1327 CTGCTCATATCCTATACATCCAGTCTAGCTAGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386
 Qy 601 GGATATGGACGGATTTCATCTTCCATCATCAGCAGTCTTGCAGGCTGAAGACCTGGCAGTT 660
 Db 1387 GGATATGGACGGATTTCATCTTCCATCATCAGCAGTCTTGCAGGCTGAAGACCTGGCAGTT 1446
 Qy 661 TATTTCTGTCCAGCAAGATTATATCTCTCCGACGTTCTGGTGGAGCCACCAAGCTGGAA 720
 Db 1447 TATTTCTGTCCAGCAAGATTATATCTCTCCGACGTTCTGGTGGAGCCACCAAGCTGGAA 1506
 Qy 721 ATCAAACGG 729
 Db 1507 ATCAAACGG 1515

RESULT 10
 AAF89733
 ID AAF89733 standard; DNA; 1796 BP.
 XX AAF89733;
 AC AAF89733;
 XX 23-JUL-2001 (first entry)
 DT Nucleotide sequence of an Ig-574 fusion protein.
 DE Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
 KW hypersensitivity; autoimmune disease; central nervous system disorder;
 KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
 KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
 KW Helicobacter-related disease; immune disorder; ss.
 XX Synthetic.
 OS Mus sp.
 XX

Key Location/Qualifiers
 FT 12..1790
 CDS /*tag= a
 FT /transl_except= (1518..1520, aa: Met)
 XX WO200136486-A2.
 PN 25-MAY-2001.
 PD 13-NOV-2000; 2000WO-GB004317.
 PF 18-NOV-1999; 99WO-GB003859.
 PR 15-FEB-2000; 2000GB-00003527.
 PR 02-MAR-2000; 2000GB-00005071.
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.
 PA Kingman A, Kingman SM, Bebbington CR, Carroll MW, Ellard FW,
 PI Myers KA;
 XX WPI; 2001-343805/36.
 DR P-PSDB; AAB83838.
 XX

Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
 XX Claim 9; Fig 6; 118pp; English.
 PS The specification describes the use of a single chain antibody (ScFv),
 XX which is capable of recognizing a disease associated molecule in the
 CC manufacture of a medicament for the prevention and treatment of a disease
 CC condition. The ScFv antibody is useful in the manufacture of a
 CC medicament, for affecting a disease in vivo, for preparing a

CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
 CC treatment of a disease. The ScFv antibody is also useful for treating
 CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
 CC diseases, cancers, central nervous system disorders including Parkinson's
 CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
 CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
 CC related diseases, and other immune disorders. The present sequence
 CC encodes an Ig-574 fusion protein
 XX
 SQ Sequence 1796 BP; 429 A; 539 C; 466 G; 362 T; 0 U; 0 Other;
 Query Match 98.9%; Score 721; DB 4; Length 1796;
 Best Local Similarity 99.3%; Pred. No. 3.3e-195;
 Matches 724; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAGGTCACAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 60
 Db 69 GAGGTCACAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 128
 Qy 61 TCCTGCAAGGCTTCGGTTACTCACTGCTGCTACTACATGCTGGTGAAGCAGAGC 120
 Db 129 TCCTGCAAGGCTTCGGTTACTCACTGCTGCTACTACATGCTGGTGAAGCAGAGC 188
 Qy 121 CATGGAAGAGCCTTGAGTGGATTGACGCTATTAACTCAACAATGCTGTACTCTCTAC 180
 Db 189 CATGGAAGAGCCTTGAGTGGATTGACGCTATTAACTCAACAATGCTGTACTCTCTAC 248
 Qy 181 AACCCAGAAATTCAGGACAAGGCCATATTAACTGTAGACAAGTCACTCCACCAAGCTTAC 240
 Db 249 AACCCAGAAATTCAGGACAAGGCCATATTAACTGTAGACAAGTCACTCCACCAAGCTTAC 308
 Qy 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGCTTATTACTGTGGAAGATCTACT 300
 Db 309 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGCTTATTACTGTGGAAGATCTACT 368
 Qy 301 ATGATTACAACTATGTTATGACTACTGGGCTCAAGTAACCTCAGTCAAGCTCTCTCA 360
 Db 369 ATGATTACAACTATGTTATGACTACTGGGCTCAAGTAACCTCAGTCAAGCTCTCTCA 428
 Qy 361 GGTGGTGGTGGAGCGGTGGTGGCGGCACTGGCGGCGGATCTAGTATTGTGATGACC 420
 Db 429 GGTGGTGGTGGAGCGGTGGTGGCGGCACTGGCGGCGGATCTAGTATTGTGATGACC 488
 Qy 421 CAGACTCCCACTTCTGCTTTCAGCAGAGACAGGGTTACCAATAACCTGCAAGGCC 480
 Db 489 CAGACTCCCACTTCTGCTTTCAGCAGAGACAGGGTTACCAATAACCTGCAAGGCC 548
 Qy 481 AGTCAGAGTGTGAGTAATGATGTAGTTGGTACCACAGAACCCAGGGCAGTCTCTTACA 540
 Db 549 AGTCAGAGTGTGAGTAATGATGTAGTTGGTACCACAGAACCCAGGGCAGTCTCTTACA 608
 Qy 541 CTGCTCATATCCTATACATCCAGTCTAGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
 Db 609 CTGCTCATATCCTATACATCCAGTCTAGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668
 Qy 601 GGATATGGACGGATTTCATCTTCCATCATCAGCAGTCTTGCAGGCTGAAGACCTGGCAGTT 660
 Db 669 GGATATGGACGGATTTCATCTTCCATCATCAGCAGTCTTGCAGGCTGAAGACCTGGCAGTT 728
 Qy 661 TATTTCTGTCCAGCAAGATTATATCTCTCCGACGTTCTGGTGGAGCCACCAAGCTGGAA 720
 Db 729 TATTTCTGTCCAGCAAGATTATATCTCTCCGACGTTCTGGTGGAGCCACCAAGCTGGAA 788
 Qy 721 ATCAAACGG 729
 Db 789 ATCAAACGG 797

RESULT 11
 AAV80295
 ID AAV80295 standard; cDNA; 2090 BP.
 XX AAV80295;
 AC AAV80295;

XX 15-MAR-1999 (first entry)
XX ScFv-IgE1 fusion construct for use in cancer gene therapy.
DE Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
XX monoclonal antibody; single chain antibody; scFv; mouse; human; IgE1; ss.
KW Mus sp.
XX Homo sapiens.
OS Synthetic.
OS Chimeric.
XX WO9855607-A2.
PN 10-DEC-1998.
XX 04-JUN-1998; 98WO-GB001627.
XX 04-JUN-1997; 97GB-00011579.
PR 20-JUN-1997; 97GB-00013150.
PR 04-JUL-1997; 97GB-00014230.
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
PA Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
PI WPI; 1999-059910/05.
XX New vector encoding a tumour interacting protein for treating cancer -
PT contains a desired nucleotide sequence and/or protein which recognises
PT tumours, and is used as a gene delivery system to treat cancer.
XX Example 13; Page 64; 82pp; English.
XX This DNA sequence encodes a fusion protein comprising the human IgE1
CC heavy constant region joined via a flexible peptide linker to an scFv
CC (see AAW86002) derived from murine 5T4 monoclonal antibody. The fusion
CC construct can be incorporated into a recombinant viral vector for use in
CC gene therapy of cancer. The trophoblast cell surface antigen defined by
CC 5T4 is expressed at high levels on the cells of a wide variety of human
CC tumours. Binding of IgE to tumour cells should promote a strong histamine
CC and hence inflammatory response and destruction of tumour cells. The
CC invention relates to a vector comprising a nucleotide sequence coding for
CC a tumour interacting protein (TIP) and optionally a nucleotide sequence
CC of interest (NOI) which encodes a protein of interest (POI), the vector
CC being capable of delivering the NOI and/or POI to the tumour recognised
CC by the TIP. Delivery can be in vivo or ex vivo
XX Sequence 2090 BP; 461 A; 653 C; 565 G; 411 T; 0 U; 0 Other;
Query Match 98.9%; Score 721; DB 2; Length 2090;
Best Local Similarity 99.3%; Pred. No. 3.5e-195;
Matches 724; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GAGGTCCAGCTTCAGCAGCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 60
DB 69 GAGGTCCAGCTGCAGCAGCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 128
QY 61 TCCTGCAAGGCTTCGGTTACTCATTTCACTGGTACTACATGACCTGGGTGAAGCAGAGC 120
DB 129 TCCTGCAAGGCTTCGGTTACTCATTTCACTGGTACTACATGACCTGGGTGAAGCAGAGC 188
QY 121 CATGGAAGAGCCTTCAGTGGATGGACCTGATTAATTAATTAATTAATTAATTAATTAATTA 180
DB 189 CATGGAAGAGCCTTCAGTGGATGGACCTGATTAATTAATTAATTAATTAATTAATTAATTA 248
QY 181 AACCAGAAATTCAGGACAGGCGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 240
DB 249 AACCAGAAATTCAGGACAGGCGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 308
QY 241 ATGGAGCTCGGACCTGCATCTGAGGACTCTGGGCTTATTACTGTGCAAGATCTACT 300
|||||

DB 309 ATGGAGCTCCGACGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368
QY 301 ATGATTAAGAACTATGTTATGAACTACTGGGTCAAGTAACCTCAGTCACCGCTCTCCTCA 360
DB 369 ATGATTAAGAACTATGTTATGAACTACTGGGTCAAGTAACCTCAGTCACCGCTCTCCTCA 428
QY 361 GGTGGTGGTGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
DB 429 GGTGGTGGTGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488
QY 421 CAGACTCCACATTCCTGCTGTTTTCAGCAGAGAGACAGGTTTACCATTAACCTGCAAGGCC 480
DB 489 CAGACTCCACATTCCTGCTGTTTTCAGCAGAGAGACAGGTTTACCATTAACCTGCAAGGCC 548
QY 481 AGTCAGAGTGTGAGTAATGATGTAGTTGGTACCAACAGAGAGCCAGGCGAGTCTCTTACA 540
DB 549 AGTCAGAGTGTGAGTAATGATGTAGTTGGTACCAACAGAGAGCCAGGCGAGTCTCTTACA 608
QY 541 CTGCTCATATCTTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
DB 609 CTGCTCATATCTTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668
QY 601 GGATATGGAGCGGATTTTCACTTTTCCATCAGCATCTTGGAGGCTGAAGACCTGGCAGTT 660
DB 669 GGATATGGAGCGGATTTTCACTTTTCCATCAGCATCTTGGAGGCTGAAGACCTGGCAGTT 728
QY 661 TATTTCTGTCAGCAAGATTATAATTTCTCTCCGAGCTTCGGTGGAGGACCAAGCTGGAA 720
DB 729 TATTTCTGTCAGCAAGATTATAATTTCTCTCCGAGCTTCGGTGGAGGACCAAGCTGGAA 788
QY 721 ATCAAACGG 729
DB 789 ATCAAACGG 797
RESULT 12
AAF89734
ID AAF89734 standard; DNA; 2090 BP.
XX AAF89734;
AC AAF89734;
XX 23-JUL-2001 (first entry)
DT Nucleotide sequence of a SvFv-IgE protein.
XX Single chain antibody; scFv; inflammatory disease; arthritis; cancer;
XX hypersensitivity; autoimmune disease; central nervous system disorder;
XX Parkinson's disease; periodontal disease; cardiopulmonary disease;
XX cardiovascular disease; gastrointestinal disorder; infection; diabetes;
XX Helicobacter-related disease; immune disorder; ss.
XX Synthetic.
OS WO200136486-A2.
XX 25-MAY-2001.
PD 13-NOV-2000; 2000WO-GB004317.
PF 18-NOV-1999; 99WO-GB003859.
XX 15-FEB-2000; 2000GB-00003527.
PR 02-MAR-2000; 2000GB-00005071.
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
PA Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
PI Myers KA;
XX WPI; 2001-343805/36.
DR Use of single chain antibody capable of recognizing a disease associated
PT molecule for manufacturing a medicament for preventing and/or treating a
PT disease condition associated with disease associated molecule.

| | | |
|----|---|--|
| XX | Example 11; Fig 7; 118pp; English. | |
| PS | The specification describes the use of a single chain antibody (ScFv), | |
| XX | which is capable of recognizing a disease associated molecule in the | |
| CC | manufacture of a medicament for the prevention and treatment of a disease | |
| CC | condition. The ScFv antibody is useful in the manufacture of a | |
| CC | medicament, for affecting a disease in vivo, for preparing a | |
| CC | pharmaceutical composition, for in vivo imaging and/or for adjuvant | |
| CC | treatment of a disease. The ScFv antibody is also useful for treating | |
| CC | inflammatory diseases including arthritis, hypersensitivity, autoimmune | |
| CC | diseases, cancers, central nervous system disorders including Parkinson's | |
| CC | disease, periodontal diseases, cardiopulmonary diseases, cardiovascular | |
| CC | diseases, gastrointestinal disorders, infections, diabetes, Helicobacter- | |
| CC | related diseases, and other immune disorders. The present sequence | |
| CC | encodes a ScFv of the invention linked to an Ige sequence | |
| XX | Sequence 2090 BP; 461 A; 654 C; 564 G; 411 T; 0 U; 0 Other; | |
| SQ | | |
| | Query Match 98.9%; Score 721; DB 4; Length 2090; | |
| | Best Local Similarity 99.3%; Pred. No. 3.5e-195; | |
| | Matches 724; Conservative 0; Mismatches 15; Indels 0; Gaps 0; | |
| Qy | 1 GAGGTCACGCTTCAGCAGCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 60 | |
| Db | | |
| Qy | 69 GAGGTCACGCTGCAGCAGCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 128 | |
| Db | | |
| Qy | 61 TCTCTGAAGGCTTCTGGTTACTCATTCACCTGGCTACTACATGCACCTGGGTGAAGCAGAGC 120 | |
| Db | | |
| Qy | 129 TCTCTGAAGGCTTCTGGTTACTCATTCACCTGGCTACTACATGCACCTGGGTGAAGCAGAGC 188 | |
| Db | | |
| Qy | 121 CATGGAAGAGCCTTCAGTGGATTGACGATTAATCCTAACAAATGGTGTACTCTCTAC 180 | |
| Db | | |
| Qy | 189 CATGGAAGAGCCTTCAGTGGATTGACGATTAATCCTAACAAATGGTGTACTCTCTAC 248 | |
| Db | | |
| Qy | 181 AACCAGAAATTCAGACAGAGCCATTAATACCTGTAGACAGTCATCCACACAGCCTAC 240 | |
| Db | | |
| Qy | 249 AACCAGAAATTCAGACAGAGCCATTAATACCTGTAGACAGTCATCCACACAGCCTAC 308 | |
| Db | | |
| Qy | 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300 | |
| Db | | |
| Qy | 309 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368 | |
| Db | | |
| Qy | 301 ATGATTACGAACATATGTTATGAGTACTGGGGTCAAGTAACTCAGTCACCGTCTCTCA 360 | |
| Db | | |
| Qy | 369 ATGATTACGAACATATGTTATGAGTACTGGGGTCAAGTAACTCAGTCACCGTCTCTCA 428 | |
| Db | | |
| Qy | 361 GGTGGTGGTGGAGCGGTGGTGGCGGCACTGGCGGGCGGATCTAGTATTGTGATGACC 420 | |
| Db | | |
| Qy | 429 GGTGGTGGTGGAGCGGTGGTGGCGGCACTGGCGGGCGGATCTAGTATTGTGATGACC 488 | |
| Db | | |
| Qy | 421 CAGACTCCACATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCAATAACCTGCAAGGCC 480 | |
| Db | | |
| Qy | 489 CAGACTCCACATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCAATAACCTGCAAGGCC 548 | |
| Db | | |
| Qy | 481 AGTCAGAGTGTGAGTAATGATGTAGTGTGGTACCAACAGAGCCAGGGCAGTCTCTCTACA 540 | |
| Db | | |
| Qy | 549 AGTCAGAGTGTGAGTAATGATGTAGTGTGGTACCAACAGAGCCAGGGCAGTCTCTCTACA 608 | |
| Db | | |
| Qy | 541 CTGCTCATATCTTATACATCCAGTCGCTAGCTGGAGTCCGTGATCGCTTCATTTGCGAGT 600 | |
| Db | | |
| Qy | 609 CTGCTCATATCTTATACATCCAGTCGCTAGCTGGAGTCCGTGATCGCTTCATTTGCGAGT 668 | |
| Db | | |
| Qy | 601 GGATATGGGACGATTTCTCTTTCCATCAGCAGCTTTCAGGCTCAAGACCTGGCAGTT 660 | |
| Db | | |
| Qy | 669 GGATATGGGACGATTTCTCTTTCCATCAGCAGCTTTCAGGCTCAAGACCTGGCAGTT 728 | |
| Db | | |
| Qy | 661 TATTTCTGTGACAGATTAATATCTCTCCGACGTTCCGTGGAGGCCACCAAGCTGGAA 720 | |
| Db | | |
| Qy | 729 TATTTCTGTGACAGATTAATATCTCTCCGACGTTCCGTGGAGGCCACCAAGCTGGAA 788 | |
| Db | | |
| Qy | 721 ATCAAAACGG 729 | |
| Db | | |

| | | |
|-----------|---|--|
| Db | 789 ATCAAAACGG 797 | |
| RESULT 13 | | |
| ADR70322 | | |
| ID | ADR70322 standard; DNA; 804 BP. | |
| XX | ADR70322; | |
| AC | ADR70322; | |
| DT | 18-NOV-2004 (first entry) | |
| XX | Poliovirus receptor (PVR)-specific scF2 coding sequence. | |
| DE | poliovirus receptor; PVR; CD155; cluster of differentiation 155; | |
| XX | receptor mediated adhesion modulation; | |
| KW | cell trafficking behaviour modulation; | |
| KW | cell invasion behaviour modulation; proliferative disorder; cancer; | |
| KW | metastasis; PVR-mediated adhesion; PVR-mediated invasion potential; | |
| KW | scFv2; gene; db. | |
| XX | Unidentified. | |
| OS | | |
| XX | Key Location/Qualifiers | |
| FT | 1..804 | |
| FT | /*tag= a | |
| FT | /partial | |
| FT | /product= "PVR-specific scFv2 protein" | |
| FT | /note= "No start codon is given" | |
| XX | | |
| PN | WO2004074324-A2. | |
| XX | | |
| PD | 02-SEP-2004. | |
| XX | | |
| XX | 19-FEB-2004; 2004WO-EP001637. | |
| XX | | |
| PR | 24-FEB-2003; 2003US-0450064P. | |
| PR | 28-MAY-2003; 2003EP-00012314. | |
| XX | | |
| PA | (XERI-) XERION PHARM AG. | |
| XX | (TUFT) UNIV TUFTS. | |
| XX | | |
| PI | Unger CM, Beste G, Zehetmeier C, Lain B, Torella C, Jay DG; | |
| PI | Eustace BK, Sloan KB; | |
| XX | WPI; 2004-652917/63. | |
| DR | P-PSDB; ADR70320. | |
| XX | | |
| PT | New molecules that modulate poliovirus receptor (PVR) mediated adhesion, | |
| PT | trafficking and/or invasion behavior of a cell expressing CD155 or PVR, | |
| PT | useful for preventing or treating proliferative disorders, such as | |
| PT | cancer. | |
| XX | | |
| PS | Claim 8; SEQ ID NO 6; 87pp; English. | |
| XX | | |
| CC | The invention comprises molecules that specifically bind to at least one | |
| CC | intra- or extracellular domain of the poliovirus receptor (PVR) - also | |
| CC | known as CD155 (cluster of differentiation 155). The molecules of the | |
| CC | invention have the ability to modulate receptor mediated adhesion, | |
| CC | trafficking and/or invasion behaviour of a cell expressing PVR. The | |
| CC | molecules of the invention are useful for the prevention and/or treatment | |
| CC | of proliferative disorders, cancer or metastasis. The molecules of the | |
| CC | invention are also useful for identifying agents that can modulate PVR- | |
| CC | mediated adhesion or invasion potential of cells. The present DNA | |
| CC | sequence encodes a PVR-specific scFv protein of the invention. | |
| XX | | |
| SQ | Sequence 804 BP; 213 A; 197 C; 227 G; 167 T; 0 U; 0 Other; | |
| | Query Match 63.6%; Score 463.6; DB 13; Length 804; | |
| | Best Local Similarity 79.8%; Pred. No. 7.5e-122; | |
| | Matches 579; Conservative 0; Mismatches 129; Indels 18; Gaps 2; | |
| Qy | 7 CAGCTTCAGCAGCTTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCTGC 66 | |
| Db | | |

Db 1 CAGCTGCAGCAGCTGTCGACCTGAGTGTGTTGAGAGCTGGGCTTCAGTGAAGATATCTCTGC 60
QY 67 AAGCTTCTGGTACTCAATTCACCTGGCTACTACATGCACTGGGTGAAGCAGCAGCATGGA 126
Db 61 AAGACTTCTGGATACACGTTCTACTGAATACACCATGCACTGGGTGAAGCAGCAGCATGGA 120
QY 127 AAGAGCCTTGAAGTGGATTGAGCAGTATTAATCCTAACAATGGTGTACTCTCTCAACCCAG 186
Db 121 AAGAGCCTTGAAGTGGATTGAGGATTTATCTTAACTGATGATAGCTACATCAACCCAG 180
QY 187 AAATTCAGCAAGGCAATTAATTAAGTGAAGATCAATCCACCAAGCTACATCAATGGAG 246
Db 181 AGGTTCAAGGGAAGGCCAATTTGACTGTAGACATCCAGCAGCAGCTACATGGAG 240
QY 247 CTGGAGCCTGACATCTGAGGACTCTGGCTTATTAATCTGTCGAAGATCTACTATGATT 306
Db 241 CTGGAGCCTTAACATCTGAGGATTTGCACTGTATTAATCTGTCGAAGATGAGCGGG--- 297
QY 307 ACGAACTATGTTATGGAATCTGAGGCTCAAGTAACTCACTCACTGCTCTCTCAGGTGGT 366
Db 298 -----GACTTGAATCTGAGGCAAGGCCACCACTCTCAAGTGTGACAGGTGGA 348
QY 367 GTGGAGAGCGGTGGTGGCGCACTGGCGCGCGGATCT-----AGTATTTGATGACC 420
Db 349 GGCGGTTTCAGGCGAGGTGCTCTGGCGGTGGCGGAAGTGCACTCGACATTTGTGATGACA 408
QY 421 CAGACTCCACATCTCTGCTGTTTTCAGCAGGAGCAGGGTTACCATTAACCTGCAAGGCC 480
Db 409 CAGTCTCCAAAATTCATGTTCCATCAGTAGGAGCAGGGTCAAGTCACTGCAAGGCC 468
QY 481 AGTCAGAGTGTGATTAATGATGTAGTGTGTTTACCAAGCAGAGCGAGCTCTCTTACA 540
Db 469 AGTCAAAATGTGGTACTAATGTAGCTGTATCAACAGAAACAGGCAATCTCTTAA 528
QY 541 CTGCTCATATCTTATACATCCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 600
Db 529 GCACTGATTTACTTCGGCATCTTACCGGTACAGTGGAGTCCCTGATCGCTTCAAGCAGT 588
QY 601 GGATATGGAGCGGATTTCACTTTTCCACATCAGCAGCTTTCAGGCTCAAGCAGTGGAGTT 660
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Db 649 TATTTCTGTGAGCAATTAACAGCTATCCGTACACGTTCCGAGGGGGACCAAGCTGGAA 708
QY 721 ATCAAA 726
Db 709 ATAAAA 714

RESULT 14
ADP85425
ID ADP85425 standard; DNA; 852 BP.
XX
AC ADP85425;
XX
DT 26-FEB-2004 (first entry)
XX
DE V1228cFv clone encoding sequence.
XX
KW Fv library; ds.
XX
OS Unidentified.
XX
PN JP200334075-A.
XX
XX 25-NOV-2003.
XX
XX 21-MAY-2002; 2002JP-00145858.
XX
XX 21-MAY-2002; 2002JP-00145858.
XX

PA (NISB) JAPAN TOBACCO INC.
XX WPI; 2004-027982/03.
DR P-PSDB; ADP85426.
XX
PT Mutated Fv library useful for screening mutated Fv for preparation of
PT mutated antibody for diagnostic purposes, having mutations at specific
PT amino acid positions of complementarity determining regions of antibody.
XX
PS Disclosure; SEQ ID NO 1; 17pp; Japanese.
XX
XX The present invention relates to mutated Fv library having mutations
CC designed such that the amino acid at position k (k is integer 2≤k≤20)
CC is introduced at amino acid position m (m is integer 2≤m≤(n-1))
CC chosen from a region consisting of n residues (n is integer 3≤n
CC contained in complementarity determining regions (CDR) or other closer
CC regions of an antibody, and forms limited Fv repository of (n) C m ×
CC ;km. The invention can be used for efficiently acquiring mutated
CC antibody. The present sequence represents V1228cFv clone encoding
CC sequence.
XX
SQ Sequence 852 BP; 208 A; 222 C; 229 G; 193 T; 0 U; 0 Other;
Query Match 61.3%; Score 446.8; DB 12; Length 852;
Best Local Similarity 77.3%; Pred. No. 4.8e-117;
Matches 563; Conservative 0; Mismatches 147; Indels 18; Gaps 1;
QY 2 AGGTCAGCTTCAGCAGTCTGACCTGACCTGGTGAAGCTGGGCTTCAGTGAAGATAT 61
Db 68 AGGTGAAACTGAGCAGTCTGAGCTGCTGTAAGCTGGGCTTCAGTGAAGATAT 127
QY 62 CCGTCAAGGCTTCTGGTACTCATTCACCTGGCTACTACATGACCTGGGTGAAGCAGGCC 121
Db 128 CTGCAAGGCTTCTGGATACACATTCACCTAGTCTGTTATGACCTGGGTGAAGCAGAAC 187
QY 122 ATGGAAAGAGCCTTCAGTGGATTGGACGCTATTAATCTTAAACAAATGGTGTACTCTCTACA 181
Db 188 CTGGCAGGCTTCAGTGGATTGGATGATGTTAATCTTACAATGATGGTATTAACCTACA 247
QY 182 ACCAGAAATTCAGAGCAAGGCCATATTAATCTGTGAGACAGTCACTCCACAGCCTACA 241
Db 248 ATGAGAAGTTCAAGGCAAGGCCACACTGACTTCAGACAAATCTCTCCAGCAGCCTACA 307
QY 242 TGGAGCTCGGAGCCTGACATCTGAGGACTCTGGCGTCTATTACCTGTGCAAGATCTACTA 301
Db 308 TGGAGCTCAGCAGCCTGACCTCTGACGACTCTGGCGTCTATTACTGTGCAAG----- 360
QY 302 TGATTAACGAATATGTTATGGACTACTGGGCTCAAGTAACTCAGTCAACCGCTCTCTCAG 361
Db 361 -----AAGGCTTGGACTATTGGGCGCAAGGACCAAGCTCAGCTCTCTCAG 409
QY 362 GTGGTGGTGGAGCGGTGGTGGCGCACTGGCGCGCGGATCTAGTATTTGTGATGACCC 421
Db 410 GTGGAGGCGCTTCAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCACTC 469
QY 422 AGACTCCACATTCCTGCTGTTTTCAGCAGAGAGCAGGTTTACCATTAACCTCAAGGCCA 481
Db 470 AGTCTCCAAATTCATGTCACATGATGAGAGCAGGCTCAGCGTCACTTCCAGAGGCCA 529
QY 482 GTCAAGTGTGAGTAAATGATGTAGTGTGGTACCAACAGAAAGCCAGGGCAGTCTCTCACAC 541
Db 530 GTCAAGTGTGGTACTTATGTAGCTGCTGATTAACAGAAACCCAGGACAAATCTCTCTAAG 589
QY 542 TGCTCATATCTATACATCCAGTCCAGTGGAGTCCCTGATGCTTCAATGGCAGTG 601
Db 590 CACTGATTTACTCGGCATCCACCGCGCACTGGAGTCCCTGATGCTTCAAGCAGTG 649
QY 602 GATATGGACGAGTTTCACTTTTCACTCAGCAGTCTTCAGGCTGAAGACCTGGCAGTTT 661
Db 650 GATCTGGGACAGATTTCACTCTCACCATTAGCAATGTGCACTCTGAAGACTTGGCAGAT 709
QY 662 ATTTCTGTGAGCAAGATTAATTTCTCTCCGAGCTTCCGTTGGAGGCCAAGCTGGAAA 721

| | | | |
|-----------|--|---|-----|
| Db | 710 | ATTTCGTGAGCAATACAGCAGCTCTCGGTATACGTTCCGGATCGGGCAACCAAGCTCGAAA | 765 |
| QY | 722 | TCAAACGG 729 | |
| | | | |
| Db | 770 | TCAAACGG 777 | |
| RESULT 15 | | | |
| AAAX01651 | | | |
| ID | AAAX01651 | standard; DNA; 1725 BP. | |
| XX | XX | | |
| AC | AAAX01651; | | |
| XX | XX | | |
| DT | 10-MAY-1999 | (first entry) | |
| XX | XX | | |
| DE | Bispecific tetraivalent antibody | BITAB724-IG10H6 DNA. | |
| XX | XX | | |
| KW | B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86; | | |
| KW | T cell activation; inhibitor; graft versus host disease; | | |
| KW | transplant rejection; allograft rejection; autoimmune disease; allergy; | | |
| KW | therapy; human; bispecific tetraivalent antibody; Bitab; | | |
| XX | BITAB7-24-IG10H6; ss. | | |
| XX | XX | | |
| OS | Mus sp. | | |
| OS | Homo sapiens. | | |
| OS | Synthetic. | | |
| OS | Chimeric. | | |
| XX | XX | | |
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| FT | | /transl_except= (pos:967..969, aa:Xaa) | |
| FT | | /note= "Xaa= Gln-Leu-Val-Gln-Val-Gln" | |
| FT | sig_peptide | 1..72 | |
| FT | | /*tag= b | |
| FT | | /note= "pebB signal sequence" | |
| FT | mat_peptide | 73..1726 | |
| FT | | /*tag= c | |
| XX | XX | | |
| PN | W09858965-A2. | | |
| XX | XX | | |
| PD | 30-DEC-1998. | | |
| XX | XX | | |
| PF | 22-JUN-1998; | 98WO-EP003791. | |
| XX | XX | | |
| PR | 20-JUN-1997; | 97EP-00870092. | |
| XX | XX | | |
| PA | (INNO-) INNOGENETICS NV. | | |
| XX | XX | | |
| PI | Lorre K, Sablon E, Buyse M, Bosman A; | | |
| XX | XX | | |
| DR | WPI; 1999-105615/09. | | |
| DR | P-PSDB; AAW90217. | | |
| XX | XX | | |
| PT | New molecules which bind B7.1 and B7.2 - useful to prevent and treat | | |
| PT | immune diseases including allograft rejection. | | |
| XX | XX | | |
| PS | Example 7.1; Fig 15; 182pp; English. | | |
| XX | XX | | |
| CC | This DNA sequence encodes the bispecific tetraivalent antibody BitabB7-24- | | |
| CC | IG10H6 (see AAW90217) comprising the anti-B7.1 murine monoclonal antibody | | |
| CC | (Mab) B7-24 VH region joined, via a flexible synthetic linker, to the B7- | | |
| CC | 24 VL region, the human IgG3 hinge region, a helix-turn-helix | | |
| CC | dimerisation domain, the human IgG3 hinge domain, the anti-B7.2 Mab 1G10 | | |
| CC | VH region, another flexible linker, the Ig10 VL region and a | | |
| CC | hexahistidine tag. The Bitab has been expressed in Escherichia coli | | |
| CC | cells. It cross-links, and/or cross-reacts, with the costimulatory | | |
| CC | molecules B7.1 and B7.2 expressed on the membrane of professional antigen | | |
| CC | -presenting cells, leading to the inhibition of antigen-specific T cell | | |
| CC | activation. The invention relates to such B7-binding molecules, methods | | |
| CC | for their production, and their use for treating or preventing diseases | | |
| CC | of the immune system, in particular graft rejection, graft versus host | | |

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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 18:41:00 ; Search time 190 Seconds
(without alignments)
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Title: US-10-016-686-5
Perfect score: 729
Sequence: 1 9aggtccagcttcagcagtc.....ccaaagctggaatcaaacgg 729

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: +
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 458.2 | 62.9 | 756 | 2 | US-08-797-689-17 |
| 2 | 458.2 | 62.9 | 756 | 4 | US-09-984-186-17 |
| 3 | 438.8 | 60.2 | 864 | 3 | US-09-423-439-47 |
| 4 | 438.8 | 60.2 | 2019 | 3 | US-09-423-439-31 |
| 5 | 438.8 | 60.2 | 2025 | 3 | US-09-423-439-37 |
| 6 | 421.6 | 57.8 | 777 | 4 | US-10-092-246-5 |
| 7 | 421.6 | 57.8 | 777 | 4 | US-10-096-246A-5 |
| 8 | 416.8 | 57.2 | 777 | 4 | US-10-092-246-7 |
| 9 | 416.8 | 57.2 | 777 | 4 | US-10-096-246A-7 |
| 10 | 413.8 | 56.8 | 723 | 4 | US-09-581-345-1 |
| 11 | 412 | 56.5 | 777 | 4 | US-10-092-246-6 |
| 12 | 412 | 56.5 | 777 | 4 | US-10-096-246A-6 |
| 13 | 410.8 | 56.4 | 717 | 3 | US-09-142-974B-1 |
| 14 | 410.8 | 56.4 | 1176 | 3 | US-09-142-974B-3 |
| 15 | 400.2 | 54.9 | 777 | 4 | US-10-092-246-4 |
| 16 | 400.2 | 54.9 | 777 | 4 | US-10-096-246A-4 |
| 17 | 399.2 | 54.8 | 774 | 4 | US-10-092-246-3 |
| 18 | 399.2 | 54.8 | 774 | 4 | US-10-096-246A-3 |
| 19 | 394.4 | 54.1 | 774 | 4 | US-10-092-246-1 |
| 20 | 394.4 | 54.1 | 774 | 4 | US-10-096-246A-1 |
| 21 | 394 | 54.0 | 726 | 2 | US-08-553-497A-25 |
| 22 | 391.8 | 53.7 | 732 | 2 | US-08-553-497A-27 |
| 23 | 391.8 | 53.7 | 732 | 2 | US-08-553-497A-19 |
| 24 | 388.6 | 53.3 | 732 | 2 | US-08-553-497A-21 |
| 25 | 388.2 | 53.3 | 1135 | 4 | US-09-203-958A-3 |
| 26 | 386.6 | 53.0 | 894 | 4 | US-09-486-814A-1 |
| 27 | 383.6 | 52.6 | 719 | 3 | US-08-279-772A-7 |

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| 28 | 383.6 | 52.6 | 720 | 3 | US-08-902-486-10 | Sequence 10, Appl |
| 29 | 382.2 | 52.4 | 717 | 4 | US-09-473-653-5 | Sequence 5, Appl |
| 30 | 382 | 52.4 | 1797 | 1 | US-08-463-163-2 | Sequence 2, Appl |
| 31 | 379.6 | 52.1 | 771 | 4 | US-09-526-738A-1 | Sequence 1, Appl |
| 32 | 379.6 | 52.1 | 780 | 4 | US-09-526-738A-3 | Sequence 3, Appl |
| 33 | 379.4 | 52.0 | 843 | 3 | US-09-423-439-43 | Sequence 43, Appl |
| 34 | 379.4 | 52.0 | 1998 | 3 | US-09-423-439-50 | Sequence 50, Appl |
| 35 | 378.4 | 51.9 | 831 | 2 | US-08-403-853-17 | Sequence 17, Appl |
| 36 | 377.4 | 51.8 | 738 | 2 | US-08-553-497A-23 | Sequence 23, Appl |
| 37 | 376.2 | 51.6 | 2012 | 1 | US-08-235-838-15 | Sequence 15, Appl |
| 38 | 376.2 | 51.6 | 2012 | 2 | US-08-465-473B-15 | Sequence 10, Appl |
| 39 | 374.4 | 51.4 | 748 | 1 | US-08-235-838-10 | Sequence 10, Appl |
| 40 | 374.4 | 51.4 | 748 | 2 | US-08-465-473B-10 | Sequence 1, Appl |
| 41 | 373.6 | 51.2 | 810 | 2 | US-08-652-507-1 | Sequence 7, Appl |
| 42 | 371.4 | 50.9 | 720 | 2 | US-08-800-198-7 | Sequence 15, Appl |
| 43 | 371.4 | 50.9 | 720 | 2 | US-09-296-595-7 | Sequence 7, Appl |
| 44 | 371.4 | 50.9 | 1679 | 2 | US-08-661-052-15 | Sequence 15, Appl |
| 45 | 371.4 | 50.9 | 1679 | 3 | US-09-188-082-15 | Sequence 15, Appl |

ALIGNMENTS

RESULT 1
US-08-797-689-17
; Sequence 17, Application US/08797689
; Patent No. 5876969
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; APPLICANT: Fournier, Alain
; APPLICANT: Guittou, Jean-Dominique
; APPLICANT: Jung, Gerard
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

; LENGTH: 777

; TYPE: DNA

; ORGANISM: mouse

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(777)

; OTHER INFORMATION: scFv protein M116-15 1 - 720

; OTHER INFORMATION: e-tag 721 - 777

US-10-096-246A-7

Query Match 57.2%; Score 416.8; DB 4; Length 777;
Best Local Similarity 74.8%; Pred. No. 6.4e-123;
Matches 543; Conservative 1; Mismatches 169; Indels 15; Gaps 1;

QY 2 AGTCCAGGCTTCAGCAGTCTGACCTGACCTGCTGTAAGCTGGGCTTCAGTGAAGATAT 61
DB 8 AGTCCAACTGCAGAGTTCAGGACCTGAGCTGTGTGAAGCTGGGCTTCAGTGAAGATAT 67
QY 62 CTGCAAGGCTTCGTGTTACTATTCACTGGCTTACTATGCACTGGGTGAAGCAGAGCC 121
DB 68 CTGCAAGGCTTCGTGCTACACCTTCACTGACTTACCATTGTTCACTGGGTGAAGGGAAGC 127
QY 122 ATGGAAGGCTTCGTGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 181
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DB 188 GTGAGACTTCAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 247
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DB 653 ATTTCTGTGAGGAAGATTAATTTCTCTCCGAGTTTCGTTGAGGAGCACCAGCTGGAAA 712
QY 722 TCAACCGG 729
DB 713 TAAACCGG 720

RESULT 10

US-09-581-345-1

; Sequence 1, Application US/09581345

; Patent No. 6809184

; GENERAL INFORMATION:

; APPLICANT: Pastan, Ira H.

; APPLICANT: Chowdhury, Partha S.
; APPLICANT: The Government of the United States
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Antibodies, Including Fv Molecules, and
; TITLE OF INVENTION: Immunoconjugates Having High Binding Affinity for
; TITLE OF INVENTION: Mesothelin and Methods for Their Use
; FILE REFERENCE: 015280-339100US
; CURRENT APPLICATION NUMBER: US/09/581,345
; PRIORITY FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/067,175
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: WO PCT/US98/25270
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SS scFv
US-09-581-345-1

Query Match 56.8%; Score 413.8; DB 4; Length 723;
Best Local Similarity 75.0%; Pred. No. 5.6e-122;
Matches 544; Conservative 1; Mismatches 174; Indels 6; Gaps 2;

QY 2 AGTCCAGGCTTCAGCAGTCTGACCTGACCTGCTGTAAGCTGGGCTTCAGTGAAGATAT 61
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QY 62 CTGCAAGGCTTCGTGTTACTATTCACTGGCTTACTATGCACTGGGTGAAGCAGAGCC 121
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QY 182 ACCAGAAATTCAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 241
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DB 305 ACGACGGGA- ---GGGGTTTTGACTACTGGGGCCAGGGACCCAGGTCACCGTCTCCTCAG 361
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Db 719 TAAAA 723
RESULT 11
US-10-092-246-6
; Sequence 6, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Monoclonal ScFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-6

Query Match 56.5%; Score 412; DB 4; Length 777;
Best Local Similarity 74.2%; Pred. No. 2.2e-121;
Matches 540; Conservative 1; Mismatches 172; Indels 15; Gaps 1;
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Db 8 AGTCCAACTGCGAGGACTGAGGACCTGAGCTGGTGAAGTCTGGGGCTTCAGTGAAGATAT 67
QY 62 CTGCAAGGCTTCGTGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121
Db 68 CTGCAAGGCTTCGTGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGGGAAGC 127
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Db 713 TAAAAACGG 720
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; Sequence 6, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Blaine
; APPLICANT: Nagata, Leslie
; APPLICANT: Alvi, Azhar Z.
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Monoclonal ScFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/096,246A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6
; LENGTH: 777
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(777)
; OTHER INFORMATION: scFv protein M116-16 1 - 720
; OTHER INFORMATION: e-tag 721 - 777
US-10-096-246A-6

Query Match 56.5%; Score 412; DB 4; Length 777;
Best Local Similarity 74.2%; Pred. No. 2.2e-121;
Matches 540; Conservative 1; Mismatches 172; Indels 15; Gaps 1;
QY 2 AGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCTGGGGCTTCAGTGAAGATAT 61
Db 8 AGTCCAACTGCGAGGACTGAGGACCTGAGCTGGTGAAGTCTGGGGCTTCAGTGAAGATAT 67
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| Qy | 542 | TGCTCATAT | CTCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTTGGCAGTG | 601 |
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| Db | 593 | GATCTGGA | ACAGATTTCACTCTCCACCATTAGCAATGTGCAGTCTGAAGACTTGGCAGATT | 652 |
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| ; Sequence 1, Application US/09142974B | | | | |
| ; Patent No. 6451995 | | | | |
| ; GENERAL INFORMATION: | | | | |
| ; APPLICANT: Cheung, Nai-Kong V. | | | | |
| ; APPLICANT: Larson, Steven M. | | | | |
| ; APPLICANT: Guo, Hong-Pen | | | | |
| ; APPLICANT: Rivlin, Ken | | | | |
| ; APPLICANT: Sadelain, Michel | | | | |
| ; TITLE OF INVENTION: Single Chain FV Constructs of Anti-Ganglioside GD2 | | | | |
| ; FILE OF INVENTION: Antibodies | | | | |
| ; FILE REFERENCE: MSK.P-013-USNP | | | | |
| ; CURRENT APPLICATION NUMBER: US/09/142,974B | | | | |
| ; CURRENT FILING DATE: 1998-09-18 | | | | |
| ; PRIOR APPLICATION NUMBER: PCT/US97/04427 | | | | |
| ; PRIOR FILING DATE: 1997-03-20 | | | | |
| ; PRIOR APPLICATION NUMBER: 60/013,703 | | | | |
| ; PRIOR FILING DATE: 1996-03-20 | | | | |
| ; NUMBER OF SEQ ID NOS: 5 | | | | |
| ; SOFTWARE: PatentIn Ver. 2.1 | | | | |
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| ; LENGTH: 717 | | | | |
| ; TYPE: DNA | | | | |
| ; ORGANISM: Murine | | | | |
| ; FEATURE: | | | | |
| ; OTHER INFORMATION: 5F11-bCFV | | | | |
| ; NAME/KEY: unsure | | | | |
| ; LOCATION: (37) | | | | |
| ; NAME/KEY: unsure | | | | |
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| US-09-142-974B-1 | | | | |
| Query Match 56.4%; Score 410.8; DB 3; Length 717; | | | | |
| Best Local Similarity 74.7%; Pred. No. 5.1e-121; | | | | |
| Matches 544; Conservative 1; Mismatches 171; Indels 12; Gaps 2 | | | | |
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| Qy | 122 | ATGGAAGAG | CCCTTGAGTGGATTTGAGCGTATTAATCTCTAAATATGGTGTACTCTCTACA | 181 |
| Db | 122 | ATGGAAGAG | CCCTTGAGTGGATTTGAGGATTTAATCTCTAAATATGGTGTACTCTCTACA | 181 |

GenCore version 5.1.6
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(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
 - 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
 - 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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 - 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 728.2 | 99.9 | 729 | 19 | US-10-334-235-1 |
| 3 | 728.2 | 99.9 | 729 | 18 | US-10-787-881A-1 |
| 4 | 727.4 | 99.8 | 1807 | 14 | US-10-060-585-2 |
| 5 | 727.4 | 99.8 | 1807 | 18 | US-10-334-235-2 |
| 6 | 727.4 | 99.8 | 1807 | 19 | US-10-787-881A-2 |
| 7 | 724.4 | 99.4 | 1467 | 18 | US-10-060-585-3 |
| 8 | 724.4 | 99.4 | 1467 | 14 | US-10-334-235-3 |
| 9 | 724.4 | 99.4 | 1467 | 19 | US-10-787-881A-3 |
| 10 | 724.2 | 99.3 | 1518 | 14 | US-10-104-522-5 |
| 11 | 724.2 | 99.3 | 1518 | 14 | US-10-060-585-5 |

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| 12 | 724.2 | 99.3 | 1518 | 18 | US-10-334-235-5 |
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| 15 | 721 | 98.9 | 2090 | 14 | US-10-104-522-6 |
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| 17 | 721 | 98.9 | 2090 | 18 | US-10-334-235-6 |
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| 19 | 505.4 | 69.3 | 729 | 19 | US-10-879-994-9 |
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| 21 | 481.2 | 66.0 | 10511 | 18 | US-10-627-649-109 |
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| 23 | 458.2 | 62.9 | 756 | 14 | US-10-237-667-17 |
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| 25 | 458.2 | 62.9 | 756 | 14 | US-10-237-866-17 |
| 26 | 458.2 | 62.9 | 756 | 14 | US-10-237-871-17 |
| 27 | 458.2 | 62.9 | 756 | 14 | US-10-237-624-17 |
| 28 | 458.2 | 62.9 | 756 | 17 | US-10-702-536-17 |
| 29 | 458.2 | 62.9 | 756 | 17 | US-10-702-636-17 |
| 30 | 439.4 | 60.3 | 759 | 9 | US-09-978-752-10 |
| 31 | 432.8 | 59.4 | 795 | 14 | US-10-114-716A-47 |
| 32 | 430.8 | 59.1 | 2952 | 18 | US-10-296-085A-30 |
| 33 | 424.4 | 58.2 | 723 | 18 | US-10-405-123-2 |
| 34 | 421.6 | 57.8 | 777 | 15 | US-10-096-246-5 |
| 35 | 418.4 | 57.4 | 774 | 17 | US-10-239-656-58 |
| 36 | 417.2 | 57.2 | 720 | 18 | US-10-482-630-52 |
| 37 | 417.2 | 57.2 | 726 | 15 | US-10-259-006A-19 |
| 38 | 417.2 | 57.2 | 726 | 18 | US-10-689-006-19 |
| 39 | 416.8 | 57.2 | 777 | 15 | US-10-096-246-7 |
| 40 | 416.8 | 57.2 | 1869 | 17 | US-10-378-832A-1 |
| 41 | 414.2 | 56.8 | 910 | 14 | US-10-104-522-1 |
| 42 | 413 | 56.7 | 1920 | 17 | US-10-120-198B-1 |
| 43 | 413 | 56.7 | 6834 | 17 | US-10-120-198B-5 |
| 44 | 412 | 56.5 | 777 | 15 | US-10-096-246-6 |
| 45 | 410.8 | 56.4 | 717 | 8 | US-08-940-544-3 |

ALIGNMENTS

RESULT 1
US-10-060-585-1
; Sequence 1, Application US/10060585
; Publication No. US20030083290A1
; GENERAL INFORMATION:
; APPLICANT: Bebbington, Alan J.
; APPLICANT: Cartoll, Miles W.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: DY023.001CPI
; CURRENT APPLICATION NUMBER: US/10/060,585
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 09/445375
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: GB 9711579.4
; PRIOR FILING DATE: 1997-06-04
; PRIOR APPLICATION NUMBER: GB 9713150.2
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: GB 9714230.1
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/GB99/03859
; PRIOR FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:


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; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence encoding 574 single chain antibody
US-10-787-881A-2

Query Match          99.8%; Score 727.4; DB 19; Length 1807;
Best Local Similarity 99.9%; Pred. No. 2.9e-224;
Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 7
US-10-060-585-3
; Sequence 3, Application US/10060585
; Publication No. US20030083290A1
; GENERAL INFORMATION:

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; APPLICANT: Kingsman, Alan J.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: DYO023.001CPI
; CURRENT APPLICATION NUMBER: US/10/060,585
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 09/445375
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: GB 9711579.4
; PRIOR FILING DATE: 1997-06-04
; PRIOR APPLICATION NUMBER: GB 9713150.2
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: GB 9714230.1
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/GB99/03859
; PRIOR FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B7-1.574.1
US-10-060-585-3
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Query Match          99.4%; Score 724.4; DB 14; Length 1467;
Best Local Similarity 99.9%; Pred. No. 2.5e-223;
Matches 725; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGTCACAGCTTCAGCAGCTGAGCCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 60
DB 739 GAGGTCACAGCTTCAGCAGCTGAGCCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 798
QY 61 TCCTGCAAGGCTTCCTGTTACTCATTCTGCTGCTACTATCATGCACTGGGTGAAGCAGAGC 120
DB 799 TCCTGCAAGGCTTCCTGTTACTCATTCTGCTGCTACTATCATGCACTGGGTGAAGCAGAGC 858
QY 121 CATGGAAGAGCCTTCAGTGGATTGGACGTATTAATCTTAACAATGGTGTACTCTCTAC 180
DB 859 CATGGAAGAGCCTTCAGTGGATTGGACGTATTAATCTTAACAATGGTGTACTCTCTAC 918
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DB 919 AACCGAAATTCAGGACAGAGCAGGCCATATTAATCTGTAGACAGTCAATCCACACAGCCTAC 978
QY 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGTCTATTACTGTGCAAGATCTACT 300
DB 979 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGTCTATTACTGTGCAAGATCTACT 1038
QY 301 ATGATTACGAACTATGTTATGAGACTATCTGGGTCAAGTAACTCAGTCAACCGTCTCTCA 360
DB 1039 ATGATTACGAACTATGTTATGAGACTATCTGGGTCAAGTAACTCAGTCAACCGTCTCTCA 1098
QY 361 GGTGGTGGTGGAGCGGTGGTGGCGCAGTGGCGGCGGATCTAGTATTGTGATGACC 420
DB 1099 GGTGGTGGTGGAGCGGTGGTGGCGCAGTGGCGGCGGATCTAGTATTGTGATGACC 1158
QY 421 CAGACTCCCACTTCCTGCTGTTTTCAGCAGGAGCAGGGTTACCAATACCTGCAAGGCC 480
DB 1159 CAGACTCCCACTTCCTGCTGTTTTCAGCAGGAGCAGGGTTACCAATACCTGCAAGGCC 1218
QY 481 AGTCAGAGTGTGAGTAATGATGTAGTGTGTTTTCAGCAGGAGCAGGGTTCCTCTACA 540
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Db 1279 CTGCTCATATCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338
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RESULT 8
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; Sequence 3, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 53268200920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US 10/060,585
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of B7-1.5T4.1
US-10-334-235-3

Query Match 99.4%; Score 724.4; DB 18; Length 1467;
Best Local Similarity 99.9%; Pred. No. 2.5e-223;
Matches 725; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GAGTTCAGCTTCAGCAGCTGACCTGAGCTGGTGGAGCCTGGGCTTCAGTGAAGATA 60
Db 739 GAGTTCAGCTTCAGCAGCTGACCTGAGCTGGTGGAGCCTGGGCTTCAGTGAAGATA 798
Qy 61 TCCTGCAAGGCTTCGTTACTCATTCCTGCTACTACATGACCTGGTGGAGCAGAGC 120
Db 799 TCCTGCAAGGCTTCGTTACTCATTCCTGCTACTACATGACCTGGTGGAGCAGAGC 858
Qy 121 CATGGAAGAGCCTTCAGTGGATGAGCTGATTAATCTCAAAATGGTGTACTCTCTAC 180
Db 859 CATGGAAGAGCCTTCAGTGGATGAGCTGATTAATCTCAAAATGGTGTACTCTCTAC 918
Qy 181 AACCAAAATTCAGCAGCAGGCAATTAATCTGTAGACATCCACCAAGCCTTAC 240
Db 919 AACCAAAATTCAGCAGCAGGCAATTAATCTGTAGACATCCACCAAGCCTTAC 978
Qy 241 ATGAGCTCCGACGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
Db 979 ATGAGCTCCGACGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy 301 ATGATTACGAACCTATGTTATGACTACTGGGCTCAAGTAACCTCAGTCACCGTCTCCCTCA 360
Db 1039 ATGATTACGAACCTATGTTATGACTACTGGGCTCAAGTAACCTCAGTCACCGTCTCCCTCA 1098
Qy 361 GGTGTTGGTGGAGCGGTGGTGGCGGCACTGGCGCGCGGATCTAGTATTGTTGATGACC 420
Db 1099 GGTGTTGGTGGAGCGGTGGTGGCGGCACTGGCGCGCGGATCTAGTATTGTTGATGACC 1158
Qy 421 CAGACTCCACATTTCTGCTTTTTCAGCAGAGACAGGTTTACCATAACCTGCAAGGCC 480
Db 1159 CAGACTCCACATTTCTGCTTTTTCAGCAGAGACAGGTTTACCATAACCTGCAAGGCC 1218
Qy 481 AGTCAGAGTGTGAGTAATGATGTAGTGTGGTACCAACAGAGCCAGGCGAGTCTCTACA 540
Db 1219 AGTCAGAGTGTGAGTAATGATGTAGTGTGGTACCAACAGAGCCAGGCGAGTCTCTACA 1278
Qy 541 CTGCTCATATCTCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCAATGGCAGT 600
Db 1279 CTGCTCATATCTCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCAATGGCAGT 1338
Qy 601 GGATATGGGACGATTTTCACTTTTCCACCATCAGCACTTTGAGGCTGAAGACCTGGCAGTT 660
Db 1339 GGATATGGGACGATTTTCACTTTTCCACCATCAGCACTTTGAGGCTGAAGACCTGGCAGTT 1398
Qy 661 TATTTCCTGTCAGCAAGATTAATAATTCCTCCGACGTTTGGTGGAGSCACCAAGCTGGAA 720
Db 1399 TATTTCCTGTCAGCAAGATTAATAATTCCTCCGACGTTTGGTGGAGSCACCAAGCTGGAA 1458
Qy 721 ATCAAA 726
Db 1459 ATCAAA 1464

RESULT 9
US-10-787-881A-3
; Sequence 3, Application US/10787881A
; Publication No. US20050032216A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingman, Susan M.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: Vector
; FILE REFERENCE: 021911-000330US
; CURRENT APPLICATION NUMBER: US/10/787,881A
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/GB98/01627
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence encoding fusion protein B7-1.5T4.1
US-10-787-881A-3

Query Match 99.4%; Score 724.4; DB 19; Length 1467;
Best Local Similarity 99.9%; Pred. No. 2.5e-223;
Matches 725; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GAGTTCAGCTTCAGCAGCTTGGACCTGAGCTGGAGCCTGGGCTTCAGTGAAGATA 60
Db 739 GAGTTCAGCTTCAGCAGCTTGGACCTGAGCTGGAGCCTGGGCTTCAGTGAAGATA 798
Qy 61 TCCTGCAAGGCTTCGTTACTCATTCCTGCTACTACATGACCTGGTGGAGCAGAGC 120
Db 799 TCCTGCAAGGCTTCGTTACTCATTCCTGCTACTACATGACCTGGTGGAGCAGAGC 858

US-10-334-235-16

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| Best Local Similarity | 99.5% | Pred. No. | 2.1e-222 | | | | |
| Matches | 725 | Conservative | 0 | Mismatches | 4 | Indels | 0 |
| Gaps | 0 | | | | | | |
| QY | 1 | GAGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCTGGGGCTTCAGTGAAGATA | 60 | | | | |
| Db | 3647 | GAGTTCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCTGGGGCTTCAGTGAAGATA | 3706 | | | | |
| QY | 61 | TCCTGCAAGGCTTCCTGGTTACTCATTCACCTGGCTACTACATGCACTGGGTGAAGCAGAGC | 120 | | | | |
| Db | 3707 | TCCTGCAAGGCTTCCTGGTTACTCATTCACCTGGCTACTACATGCACTGGGTGAAGCAGAGC | 3766 | | | | |
| QY | 121 | CATGGAAGAGCCTTGAGTGGATTGAGCACTTAATCCTAACATGGTGTACTCTCTAC | 180 | | | | |
| Db | 3767 | CATGGAAGAGCCTTGAGTGGATTGAGCACTTAATCCTAACATGGTGTACTCTCTAC | 3826 | | | | |
| QY | 181 | AACCAAGAAATTCAGGACAAGGCCATATTAACCTGTAGCAAGTCATCCACACAGCCTAC | 240 | | | | |
| Db | 3827 | AACCAAGAAATTCAGGACAAGGCCATATTAACCTGTAGCAAGTCATCCACACAGCCTAC | 3886 | | | | |
| QY | 241 | ATGAGCTCCGACGCTTGAATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT | 300 | | | | |
| Db | 3887 | ATGAGCTCCGACGCTTGAATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT | 3946 | | | | |
| QY | 301 | ATGATTACGAACATATGTTATGGACTCTGGGTCAAGTAACTCAGTCAAGCTCTCTCA | 360 | | | | |
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| QY | 361 | GGTGGTGGTGGGAGCGGTGGCGGCACCTGGCGGGCGCGGACTAGTATGTGATGACC | 420 | | | | |
| Db | 4007 | GGTGGTGGTGGGAGCGGTGGCGGCACCTGGCGGGCGCGGACTAGTATGTGATGACC | 4066 | | | | |
| QY | 421 | CAGACTCCACATTCCTGCTGTTTTCAGCAGGAGACAGGGTTACCTGCAAGGCC | 480 | | | | |
| Db | 4067 | CAGACTCCACATTCCTGCTGTTTTCAGCAGGAGACAGGGTTACCTGCAAGGCC | 4126 | | | | |
| QY | 481 | AGTCAGAGTCTGAGTAATGATGTAGDTTGTGTACCACAGAAAGCCAGGCGAGTCTCTTACA | 540 | | | | |
| Db | 4127 | AGTCAGAGTCTGAGTAATGATGTAGDTTGTGTACCACAGAAAGCCAGGCGAGTCTCTTACA | 4186 | | | | |
| QY | 541 | CTGCTCATATCTTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT | 600 | | | | |
| Db | 4187 | CTGCTCATATCTTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT | 4246 | | | | |
| QY | 601 | GGATATGGGACGATTTCACTTTTCAATCAGCACATTTGCAGGCTGAAGACCTTGGCAGTT | 660 | | | | |
| Db | 4247 | GGATATGGGACGATTTCACTTTTCAATCAGCACATTTGCAGGCTGAAGACCTTGGCAGTT | 4306 | | | | |
| QY | 661 | TATTTCTGTGAGCAAGATATAATTTCTCTCCGACGTTTGGTGGAGGCACCAAGCTGGAA | 720 | | | | |
| Db | 4307 | TATTTCTGTGAGCAAGATATAATTTCTCTCCGACGTTTGGTGGAGGCACCAAGCTGGAA | 4366 | | | | |
| QY | 721 | ATCAAAACGG | 729 | | | | |
| Db | 4367 | ATAAAAACGG | 4375 | | | | |

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; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCI/GB98/01627
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: GB9711579.4
; PRIOR FILING DATE: 1997-06-04
; PRIOR APPLICATION NUMBER: GB9713150.2
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: GB9714230.1
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2090
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5T4 scFv-human Ige fusion construct
US-10-104-522-6

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| Query Match | 98.9% | Score 721 | DB 14 | Length 2090 |
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| Best Local Similarity | 99.3% | Pred. No. 3.6e-222 | | |
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| QY 1 | GAGGTCCAGCTTTCAGCAGTCTGAGCCTGAGCCTGCTGAGCCTGGGGCTTCAGTGAAGATA | 60 | | |
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| QY 61 | TCTCTCAAGGCTTCTGGTTACTTCATTTCACTGGCTACTACATGCACCTGGGTGAAGCAGAGC | 120 | | |
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| QY 121 | CATGGAAAGAGCCTTGAGTGGATTTGAGCTATTAATCTTAACCAATGGTGTACTCTCTAC | 180 | | |
| DB 189 | CATGGAAAGAGCCTTGAGTGGATTTGAGCTATTAATCTTAACCAATGGTGTACTCTCTAC | 248 | | |
| QY 181 | RACCCAGAAATTCAGGACCAAGGCCATATTAACCTGTAGACAAGTCATCCACCACAGCCTAC | 240 | | |
| DB 249 | AACCCAGAAATTCAGGACCAAGGCCATATTAACCTGTAGACAAGTCATCCACCACAGCCTAC | 308 | | |
| QY 241 | ATGGAGCTCCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT | 300 | | |
| DB 309 | ATGGAGCTCCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT | 368 | | |
| QY 301 | ATGATTACAACTATGTTATGAGTACTCTGGGGTCAAGTAACTTCAGTCACCGTCTCTCA | 360 | | |
| DB 369 | ATGATTACAACTATGTTATGAGTACTCTGGGGTCAAGTAACTTCAGTCACCGTCTCTCA | 428 | | |
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| DB 429 | GGTGTGTGGAGGGGTGTGGGGGCACTGGGGGGGGGGATCTAGTATTGTGATGACC | 488 | | |
| QY 421 | CAGACTCCCACTTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATACCTGCAAGGCC | 480 | | |
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| QY 601 | GGATATGGAGCGGATTTTCACTTTCCATCAGCAGTCTTCAGGCTGAAACCTGGCAGTT | 660 | | |
| DB 669 | GGATATGGAGCGGATTTTCACTTTCCATCAGCAGTCTTCAGGCTGAAACCTGGCAGTT | 728 | | |
| QY 661 | TATTTCTCTCAGCAAGATTAATTTCTCTCCGACGTTTCGGTGGAGGACCACCAAGCTGGA | 720 | | |
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Db 789 ATCAACGG 797

Search completed: March 15, 2005, 00:12:29
Job time : 577 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 18:20:07 ; Search time 3220 Seconds
(without alignments)
8617.656 Million cell updates/sec

Title: US-10-016-686-5
Perfect score: 729
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_hic:*
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6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| C 4 | 282.4 | 38.7 | 1010 | 5 | BQ921928 AGENCOURT |
| C 5 | 280.8 | 38.5 | 594 | 2 | BE309592 |
| C 6 | 273.8 | 37.6 | 724 | 2 | BF168514 601775412 |
| C 7 | 272.2 | 37.3 | 769 | 2 | BF168856 |
| C 8 | 270 | 37.0 | 507 | 7 | BF015548 yv23a08.Y |
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| C 18 | 260 | 35.7 | 672 | 7 | CK633068 |
| C 19 | 260 | 35.7 | 672 | 7 | CK633068 AM3-AP001 |
| C 20 | 259.6 | 35.6 | 640 | 5 | BQ109114 imagesc 6 |
| C 21 | 259.2 | 35.6 | 899 | 4 | BG973020 602838676 |
| C 22 | 251.6 | 34.5 | 506 | 6 | CA578474 |
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| C 24 | 251.6 | 34.5 | 823 | 7 | CK632348 AM0-AM000 |

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ACCESSION CK629396
VERSION CK629396.1 GI:45753871
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoidea; Apoidea; Apidae; Apis.
REFERENCE 1 (bases 1 to 872)
Nunes, F.M.F., Valente, V., Sousa, J.P., Cunha, M.A.V., Pinheiro, D.G., Maia, R.M., Araujo, D.B., Costa, M.C.R., Martins, W.K., Carvalho, A.F., Monesi, N., Nascimento, A.M., Peixoto, P.M.V., Silva, M.F.R., Ramos, R.G.P., Reis, L.F.L., Dias Neto, E., Souza, S.J., Simpson, A.J.G., Zago, M.A., Soares, A.E.E., Bitondi, M.M.G., Espresafico, E.M., Espindola, F.S., Paco-Larson, M.L., Simoes, Z.L.P., Hartfelder, K. and Silva, W.A. Jr.
Open reading frame ESTs - an efficient strategy for analysis of the honey bee transcriptome
Unpublished (2004)
Contact: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Department of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonj@usp.br
This sequence was derived from the FAPESP Genome Program
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High quality sequence stop: 625.
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JOURNAL
COMMENT
TITLE
FEATURES
ORIGIN
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REFERENCE 1 (bases 1 to 1104)
Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espreafico,E.M.,
Bepindola,F.S., Peco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
Silva,W.A. Jr.
Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
Unpublished (2004)
Contact: Silva Jr., W. A.
Molecular Genetic and Bioinformatics Laboratory
Department of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br
This sequence was derived from the FAPESP Genome Program
High quality sequence start: 64
High quality sequence stop: 594.
Location/Qualifiers
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/mol_type="mRNA"
/strain="Africanized"
/db_xref="taxon:7460"
/sex="female, worker"
/dev_stage="adult"
/clone_lib="AA0023"
/note="Organ: whole body"

ORIGIN
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Best Local Similarity 68.2%; Pred. No. 3.5e-74;
Matches 452; Conservative 1; Mismatches 203; Indels 7; Gaps 4;
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QY 127 AAGAGCCTTGAGTGGATTGCAAGTATTAATCTTAACAATGGTGTACTCTTACACACGAG 186
DB 687 AAGGGACTTGAGTGGATTGGATGGATTTTCTCGGAGAGGGGAGTACTGAATACATATGAG 628
QY 187 AAATTCAGGACGAAGCCCATATTAACTGTAGACAAGTCACTCAACACAGCCTACATGGAG 246
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QY 427 CCACATTTCTGCTGTTTTCAGCAGGAGACAGGTTTACCATAACCTTGCAGGCGCAGTCAAG 486
DB 389 CCAGCAATCATGCTGCATCTCCAGGAGAGGGTCAACATGACCTGCGTGCAGTGCACCTCA 330
QY 487 AGTGTAGTAAATGATAGTGGTACCAACAGAACGCCAGGCGAGTCTCTTACATCTGCTC 546
DB 329 AGTATACG---TTACATATATTTGGTACCAACAGAGCCTGGATCTCTCCCGACAGCTCTG 273
QY 547 ATATCTTATACATCCAGTCCGCTACGCTGGAGTCCCTGATCGCTTCAATTTGGCAGTGGAT 606
DB 272 ATTTATGACACATCCAACTGGGCTCTCTGGAGTCCCTTTTCGCTTTCAGTGGCAGTGGTCT 213

QY 607 GGGAGCGATTTCACCTTTCACCATCAGCACTTTGCGAGGCTGAGACCTGGCAGTTTATTTTC 666
DB 212 GGGAGCTCTTATTTCTCTCACAATCAACCAATGGAGGCTGAGGATGCTGCCACTTATTTAC 153
QY 667 TGTACAGCAAGATTATAATTTCTCTCCGACGTTTCGGTGGAGGACCAACGCTGGAAATCAAA 726
DB 152 TCCAGGAGTGGAGTGGTTATCCGTACAGTTCCGAGG--GGGACCCAGCTGGAGCTGAAA 94
QY 727 CGG 729
DB 93 CGG 91

RESULT 4
BQ921928
LOCUS
DEFINITION
BQ921928 1010 bp mRNA linear EST 20-AUG-2002
IMAGE:6475284 5', mRNA sequence.
ACCESSION
BQ921928.1 GI:223336959
VERSION
BQ921928.1
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1010)
AUTHORS
NIH-MGC http://mgc.nhl.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM14013 row: m column: 13
High quality sequence stop: 608.
Location/Qualifiers
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/mol_type="mRNA"
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/clone="IMAGE:6475284"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1; NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 38.7%; Score 282.4; DB 5; Length 1010;
Best Local Similarity 87.9%; Pred. No. 6.8e-74;
Matches 320; Conservative 0; Mismatches 41; Indels 3; Gaps 1;
QY 1 GAGGTCCAGCTTCAGCAGTCTGACCTGACCTGGTGAAGCCCTGGGCTTCAGTGAAGATA 60
DB 69 GAGGTCCAGCTTCAGCAGTCTGAGACCTGAGATGGTGAAGCCTGGGCTTCAGTGAAGATA 128
QY 61 TCTCTCAAGGCTTCGTGTTACTTCATTCTACTGCTACTACATGCTGGGTGAAGCAGAGC 120
DB 129 TCTGCAAGGCTTCGTGATACACATTCAGTCTACTACATGCTGGGTGAAGCAGAGC 188
QY 121 CATGGAAGAGGCTTCGAGTGGATTGACGTTATTAATCTTAACAATGGTGTACTCTCTAC 180
DB 189 CATGGAAGAGGCTTCGAGTGGATTGACGTTATTAATCTTAACAATGGTGAAGTAGGTAT 248
QY 181 AACCGAATTCAGGACCAAGGCCATTAATCTGTAGACAAGTCATCCACCACAGCTTAC 240

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Db      249  AACGAGAAGTCGAGGCGAAGGCCACATTCGATGTTGACAAATCCTCCACACAGCCTAC 308
Qy      241  ATGAGATCCGCGACCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
Db      309  ATGAGCTCAACAGCCCTGACATCTGAGGACTCTGCGGTCTACTACTGTGCGATATCCAT 368
Qy      301  ATGAT---TACGAATATGTTATGGACTACTCTGGGGTCAAGTAACCTCAGTCACCGTCTCC 357
Db      369  AGGATCGGAGATFACATGCTATGGACTACTTGGGTCAAGGAACCTCAGTCACCGTCTCC 428
Qy      358  TCAG 361
Db      429  TCAG 432

RESULT 5
BE309592
LOCUS    601094848F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3489635 5',
DEFINITION mRNA sequence.
ACCESSION BE309592
VERSION    BE309592.1 GI:9168025
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 594)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
           cDNA Library Preparation: Life Technologies, Inc.
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: L1AM8530 row: 0 column: 12
           High quality sequence stop: 591.
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                 /db_xref="taxon:10090"
                 /clone="IMAGE:3489635"
                 /tissue_type="tumor, gross tissue"
                 /dev_stage="7 months"
                 /lab_host="DH10B"
                 /clone_lib="NCI CGAP Mam5"
                 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
                 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
                 Library constructed by Life Technologies. Investigators
                 providing samples: Lothar Hennighausen/Robin Humphreys,
                 NIH"

ORIGIN
Query Match      38.5%; Score 280.8; DB 2; Length 594;
Best Local Similarity 91.7%; Pred. No. 1.8e-73;
Matches 297; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy      406  AGTATTGTGATGATCCAGATCCCATCTCTGTTGTTTCAGCAGGAGCAGGTTACC 465
Db      47  AATGTTGTGATGATCCAGATCCCATCTCTGTTGTTTCAGCAGGAGCAGGTTACC 106
Qy      466  ATAACTGCAAGCCAGTCAGAGTGTGAGTAATGATGTAGTTGGTACCAACAGAGCCA 525
Db      107  ATAACTGCAAGCCAGTCAGAGTGTGAGTAATGATGTAGTTGGTACCAACAGAGCCA 166
Qy      526  GGGCAGTCTCCTACATGCTCATATCCTATACATCCAGTCGGTACGCTGGAGTCCCTGAT 585

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Db      167  GGGCAGTCTCCTAAACTTCTGATATACTATGATCCATCGTACACTGGAGTCCCTGAT 226
Qy      586  CGCTTCATTGGCAGTGGATATGGGACCGGATTTCACTTTCCACATCAGCACTTTGAGGCT 645
Db      227  CGCTTCAGTGGCAGTGGATATGGGACCGGATTTCACTTTCCACATCAGCACTTTGAGGCT 286
Qy      646  GAAGACCTGGCAGTGTATTTCTGTGTCAGCAAGATTATATCTCTCCGACGTTCCGTTGA 705
Db      287  GAAGACCTGGCAGTGTATTTCTGTGTCAGCAAGATTATAGTCTCTCCGTACACGTTCCGAGG 346
Qy      706  GGCACCAAGCTGGAATCAAAACGG 729
Db      347  GGGACCAAGCTGGAATCAAAACGG 370

BF168514
601775412F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017075 5',
DEFINITION mRNA sequence.
ACCESSION BF168514
VERSION    BF168514.1 GI:11048866
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 724)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Gilbert Smith, Ph.D.
           cDNA Library Preparation: Life Technologies, Inc.
           DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
           Clone distribution: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: L1AM9265 row: h column: 04
           High quality sequence stop: 661.
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                 /clone="IMAGE:4017075"
                 /tissue_type="spontaneous tumor, metastatic to mammary.
                 Stem cell origin."
                 /lab_host="DH10B"
                 /clone_lib="NCI CGAP Lu29"
                 /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
                 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
                 Library constructed by Life Technologies. Investigator
                 providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match      37.6%; Score 273.8; DB 2; Length 724;
Best Local Similarity 87.3%; Pred. No. 2.5e-71;
Matches 315; Conservative 0; Mismatches 31; Indels 9; Gaps 1;

Qy      1  GAGGTCCAGCTTCACAGCTCGGACCTGAGCTGAGGCTGGGCTTCAGTGAAGATA 60
Db      95  GAGGTCCAGCTTCACAGCTCGGACCTGAGCTGAGGCTGGGCTTCAGTGAAGATA 154
Qy      61  TCCTGCAAGGCTTCGTGTTACTTCATTTCACTGGCTACTACATGCATCGGCTGAAGCAGAC 120
Db      155  TCCTGCAAGGCTTCGTGTTACTTCATTTCACTGGCTACTACATGCATCGGCTGAAGCAAGT 214
Qy      121  CATGGAAGAGCCTTGAGTGGATGGAGTATTAATCTTAACATGGTGTACTCTCTAC 180

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Db      215  CCTGAAAGAGCCTTGGTGGATTGGAGAGATTAACTCTAGCACTGGTGGTACTACCTAC 274
QY      181  AACGAGAAATTCAGGACCAAGGCATATTAACTGTAGACAAGTCATCCACCAAGCCTAC 240
Db      275  AACGAGAAGTTCAGGCGCAAGGCCACATTCAGTGTAGACAATCTCTCCAGCACAGCCTAC 334
QY      241  ATGGAGCTCGGACGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
Db      335  ATGCAGCTCAAGAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGA----- 388
QY      301  ATGATTACCAACTATCTTATGAGTACTCTGGGCTCAAGTCAAGTCAAGTCAAGTCAAGTCA 360
Db      389  ---AGTACATCAGGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCAAGCCTCTCTCA 445
QY      361  G 361
Db      446  G 446

RESULT 7
BF168856
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 769)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9265 row: k column: 04
High quality sequence stop: 678.
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Location/Qualifiers
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/clone="IMAGE:4017147"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

Query Match 37.3%; Score 272.2; DB 2; Length 769;
Best Local Similarity 87.0%; Pred. No. 7.7e-71;
Matches 314; Conservative 0; Mismatches 38; Indels 9; Gaps 1;

QY      1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 60
Db      99  GAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGCTTCAGTGAAGATA 158
QY      61  TCCTGCAAGGCTTCTGGTTACTCAATTCAGTGGCTACTACATGCACTGGGGAAGCAGAGC 120

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Db      159  TCCTGCAAGGCTTCTGGTTACTCAATTCAGTGGCTACTACATGCACTGGGTGAAGCAAGT 218
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Db      219  CTTGAAAGAGAGCCTTGGTGGATTGGAGAGATTAACTCTAGCACGGTGGTACTACCTAC 278
QY      181  AACGAGAATTCAGGACCAAGGCCATATTAACTGTAGACAAGTCATCCACCAAGCCTAC 240
Db      279  AACGAGAAGTTCAGGCGCAAGGCCACATTCAGTGTAGACAATCTCTCCAGCACAGCCTAC 338
QY      241  ATGGAGCTCGGACGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
Db      339  ATGCAGCTCAAGAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGA----- 392
QY      301  ATGATTACCAACTATCTTATGAGTACTCTGGGCTCAAGTCAAGTCAAGTCAAGTCAAGTCA 360
Db      393  ---AGTACATCAGGGCTATGGACTACTGCGGTCAAGGAACCTCAGTCAAGCCTCTCTCA 449
QY      361  G 361
Db      450  G 450

RESULT 8
BF015548
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 507)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

MGI:1421142
Seq primer: -40RP from Gibco
High quality sequence stop: 456.
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/clone="IMAGE:3660374"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

Query Match 37.0%; Score 270; DB 2; Length 507;

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Best Local Similarity 85.5%; Pred. No. 3.2e-70;
Matches 313; Conservative 0; Mismatches 50; Indels 3; Gaps 1;

QY 1 GAGTCCAGCTTCAGCAGCTTCGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 60
Db 92 GAGGTCAGCTGCAACAGCTCTGACCTGAGCTGGTGAAGCCTGGGCTTCAGTGAAGATA 151
QY 61 TCCTGCAAGGCTTCGTGTTACTCATTCACCTGGCTACTACATGACCTGGGGTGAAGCAGAGC 120
Db 152 TCCTGCAAGGCTTCGTGTTACTCATTCACCTGGCTACTACATGACCTGGGGTGAAGCAGAGC 211
QY 121 CATGGAAGAGCTTCGAGTGGATGAGACGTATTAACTCCTAACCAATGGTGTACTCTCTAC 180
Db 212 CATGGAAGAGCTTCGAGTGGATGAGACGTATTAACTCCTAACCAATGGTGTACTCTCTAC 271
QY 181 AACCGAAGATTCAGGACAGGCGCATATTAACTGTAGACAGTCAATCCACACAGCCTAC 240
Db 272 AACCGAAGATTCAGGACAGGCGCATATTAACTGTAGACAGTCAATCCACACAGCCTAC 331
QY 241 ATGGAGCTCCGCGAGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCT--- 297
Db 332 ATGGAGCTCAACAGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATTTAC 391
QY 298 ACTATGATACGAACATGATGAGTATGAGTACTGCGGTCAAGTAACTGACGTCACCGTCTCC 357
Db 392 TACAGTGGTAGCTACTGCTGATCTGATGCTGCGGCGCAGGACCAACGCTCACCGTCTCC 451
QY 358 TCAGGT 363
Db 452 TCAGCT 457

RESULT 9
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LOCUS AM1-AA0014-041102-021-H09-AA0014 Apis mellifera cDNA, mRNA
DEFINITION
sequence.
CK629415
VERSION CK629415.1 GI:45753890
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera
REFERENCE 1 (bases 1 to 1419)
AUTHORS Nunes, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G.,
Maia, R.M., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F.,
Monesi, N., Nascimento, A.M., Peixoto, P.M.V., Silva, M.F.R.,
Ramos, R.G.P., Reis, L.F.L., Dias Neto, E., Souza, S.J., Simpson, A.J.G.,
Zago, M.A., Soares, A.E.E., Bitondi, M.M.G., Espresafico, E.M.,
Espindola, F.S., Paco-Larson, M.L., Simoes, Z.L.P., Hartfelder, K. and
Silva, W.A. Jr.
Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
Unpublished (2004)
Contact: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Departamento de Genetica, FMRP/USP, FUNDHERP
Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br
This sequence was derived from the FAPESP Genome Program
High quality sequence start: 63
High quality sequence stop: 605.
FEATURES
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/mol_type="mRNA"
/strain="Africanized"
/db_xref="taxon:7460"
/sex="female, worker"

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/dev_stage="adult"
/clone_lib="AA0014"
/note="Organ: whole body"

ORIGIN
Query Match 37.0%; Score 269.4; DB 7; Length 1419;
Best Local Similarity 68.8%; Pred. No. 6.7e-70;
Matches 427; Conservative 1; Mismatches 185; Indels 8; Gaps 4;

QY 108 GGTGAAGCAGAGCCATGGAAGAGCCTTCAGTGGATTTGACGTATTATTCCTAACAAATGG 167
Db 703 GGTGAAGCAGAGCCCTGNAACAG-GACTTGGAGTGGATTGGATG-ATTTTCTCTGGAGAGG 646
QY 168 TGTACTCTCTCAACACGAAATTCAGGACAAGGCCATATTAACTGTAGACAAGTCATC 227
Db 645 ANGTAAGTCTGATACATGAGAGTTCAAGGGCAGGACACACACTGAGTGTAGACAAGTCCTC 586
QY 228 CACCAAGCCTACATGGAGCTCCGAGCCTGACATCTGAGGACTCTGCGGTCTATTACTG 287
Db 585 CAGCAGAGCTATATGGAGCTCACTAGGCTGACATCTGAGGACTCTGCTGTCTATTCTG 526
QY 288 TCGAAGATCTACTATGATTAACGAATATGTTATGACTACTGGGTCAAGTAACTCCTCAGT 347
Db 525 TGCTAGAGGGGACTACTATAGCGCTACTTT---GACTTTGTGGGGCCAAAGGACCAACG 469
QY 348 CACCGTCTCTCAGGTGGTGGAGCGGTGGTGGCGGCACTGGCGGCGCGGATCTAG 407
Db 468 CACCGTCTCTCATGTGGAGACGGTTCAAGCGGAGGTGGCTCTGTCCGTGGCGGATCTGA 409
QY 408 TATTGTGATGACCCAGACTCCCAATTCCTGTTGTTTCAGAGAGAGAGAGGTTTACCAT 467
Db 408 CATTGAGCTCACCCAGTCTCCAGCAATCATGTCTCATCTCCAGGGGAGAGGTTCAACAT 349
QY 468 AACCTGCAAGGCGCTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGCCAGG 527
Db 348 GACCTGCGAGTGGCAGCTCAAGTATACGTTTACA---TATATTGTACCAACAGAGCCTGG 292
QY 528 GCAGTCTCCTACACTGCTCATATCCTATACATCCAGTCCGCTACGCTGGAGTCCCTGATCG 587
Db 291 ATCTCTCCCCAGACTCCTGATTTATGACACATCCAAAGTGGCTCTCTGGAGTCCCTTTTCG 232
QY 588 CTTCAATTGCGAGTGAATATGGACCGGATTTCACTTTACCATCAGACACTTTTCAGAGCTGA 647
Db 231 CTTCAAGTGGCAGTGGGCTCTGGGACCTCTTATTCTCTCAAAATCAACCGAATGGAGGCTGA 172
QY 648 AGACCTGGCAGTTTATTCTGTGCACAAAGATTATAATTCTCTCCGAGCTTCGGTGGAGG 707
Db 171 GGATGCTGCCACTTATTACTGCCAGAGTGGAGTGCTTATCCGTACACGTTCCGGAGGGGG 112
QY 708 CACCAAGCTGGAATCAAAACG 728
Db 111 GACCAAGCTGGAGCTGAAACG 91

RESULT 10
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LOCUS 602093730F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208022 5',
DEFINITION mRNA sequence.
ACCESSION BF580610
VERSION BF580610.1 GI:11654322
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 883)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

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| | |
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| TITLE | Epindola,F.S., Paco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and Silva,W.A. Jr. |
| JOURNAL | Open reading frame ESTs - an efficient strategy for analysis of the honey bee transcriptome |
| COMMENT | Unpublished (2004) Contact: Silva Jr, W. A. Molecular Genetic and Bioinformatics Laboratory Department of Genetics, FMRP/USP, FUNDHERP Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil Tel: +55 16 396393300 Fax: +55 16 39639309 Email: wilsonjr@usp.br This sequence was derived from the FAPESP Genome Program High quality sequence start: 62 High quality sequence stop: 662. |

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FEATURES
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      /dev_stage="adult"
      /clone_lib="AA0014"
      /notes="Organ: whole body"

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  Best Local Similarity 67.8%;   Pred. No. 2.1e-68;
  Matches 431; Conservative 1; Mismatches 198; Indels 8; Gaps 4;

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| 721 | Db | TATGATATAGCCTCGGTGAGCAGAAAGCCTGAACAGGACCTTGAGTGGACTGGAATCGAT | 662 |
| 153 | QY | TAAATCCTAAACAATGGTGTATCTCTCAACCAAGAAATTCAGGACAAGGCCATATTAAC | 212 |
| 661 | Db | TTTTCTCGAGAGGGGAGTACTGAATACAAATGAGAAAGTTCAAGGGCAGGGCCACACTGAG | 602 |
| 213 | QY | T--GTAGACAAGTCATCCACACAGCCTACATGAGAGCTCCGACGCCCTGACATCTGAGGACT | 271 |
| 601 | Db | TGGTAGACAAGTCTCCAGCAGAGCCTATATGAGAGTCTACTAGGCTGACATCTGAGACT | 542 |
| 272 | QY | CTCGGGTCTATTACTGTGCAAGATCTACTATGANTATAGAACTATGATATGGACTACTGGG | 331 |
| 541 | Db | CTGCTGTCTATTCTGTGTAGAGGGGACTACTATAGGGCGCTACTTT--GACTTTGGG | 485 |
| 332 | QY | GTCAAGTAAACCTCAGTCACCGTCTCTCTCAGGTGGTGGTGGAGCGGTGGTGGGGGACATG | 391 |
| 484 | Db | TCCMAGGGACCAAGGTCAAGTCTCTCTCATGTGGAGCGGTTCAAGGGGAGGTGGCTCTG | 425 |
| 392 | QY | GGGGGGCGGATCTAGTATTGTGATGAGCCAGACTCCCAATTCCTGCTGTGTTTCAGCAG | 451 |
| 424 | Db | GGGGTGGCGGATCTGATCTGTAGTACTCAAGTCTCCAGCAATCATGTCTGCACTCTCCAG | 365 |
| 452 | QY | GAGACAGGGTTACCAATTAACCTGCAAGGCCAGTCAGAGTGTGAGTAAATGATGTAGDTTGGT | 511 |
| 364 | Db | GGGAGAGGTTCAACCATGACCTGCAGTGCACGCTCAAGTATACGTTACA--TATATTGGT | 308 |
| 512 | QY | ACCAACAGAGCAGCGGAGTCTCTACACTGCTCATATCTCTATATACATCCAGTCCGCTACG | 571 |
| 307 | Db | ACCAACAGAAAGCGTGGATCCTCCCCAGACTCCTGATTTTATGACACATCAACAGTGGCTC | 248 |
| 572 | QY | CTGGAGTCCCTGATCGCTTTCATTGGCAGTGGGATATGGGACGGATTTCACTTTCAACATCA | 631 |
| 247 | Db | CTGGAGTCCCTTTTCGCTTTCAGTGGCAGTGGGTCTGGGACCTCTATTCTCTCACANTCA | 188 |
| 632 | QY | GCATTTGCAAGCTGAGACCTGGCAGTTTATTCTGTCAGCAAGATTAATATCTCCTC | 691 |
| 187 | Db | ACCGAATGGAGGCTGAGGATGCTGCCACTATTACTGCGCAGAGTGGAGTGGTTATCCGT | 128 |
| 692 | QY | CGACGTTCCGTTGGAGGCACCAAGCTGGAAATCAAACGG | 729 |

127 ACACGTTCCGAGGGGGGACCAAGCTGGAGCTGAAACGG 90

RESULT 13

BI104341

LOCUS

DEFINITION

602889919F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5035013 5', mRNA linear EST 26-JUN-2001

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BI104341.1 GI:14555234

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 598)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: <http://image.lnl.gov>

Plate: LLAM11097 row: f column: 06

High quality sequence stop: 598.

Location/Qualifiers

1. 598

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/mol_type="mRNA"

/strain="CZECH II"

/db_xref="taxon:10090"

/clone="IMAGE:5035013"

/tissue_type="spontaneous tumor, metastatic to mammary."

stem cell origin."

/lab_host="DHL08"

/clone_lib="NCI_CGAP_Lu29"

/note="Organ: lung; Vector: pCMV-Sport6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

FEATURES

source

[illegible]

Db 392 GGTTACGGGGTGGGGCCCTACTACTTGTGACTCTGGGGCCAGGCACCTATCACA 451
Qy 352 GTCTCTCTCAG 361
Db 452 GTCTCTCTCAG 461

RESULT 14
BX969451
LOCUS
DEFINITION
Chromosome engineering clone MHPN79016, genomic survey sequence.
ACCESSION
BX969451
VERSION
BX969451.1 GI:49700874
KEYWORDS
GSS; genome survey sequence; MICEP.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 842)
ADAMS, D.J., BIGGS, P.J., COX, A.V., DAVIES, R.M., VAN DER WEYDEN, L.,
JONKERS, J., SMITH, J., PLUMB, R.W., TAYLOR, R.G., NISHIJIMA, I., YU, Y.,
ROGERS, J. and BRADLEY, A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. <http://www.sanger.ac.uk/MICEP>
FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN79016"
/clone_lib="MHPN"

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Best Local Similarity 93.2%; Pred. No. 9.9e-68;
Matches 274; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy 1 GAGGTCAGCTTCAGCAGCTGCGACCTGCTGGAAGCCTGGGCTTCAGTGAAGATA 60
Db 284 GAGGTCAGCTGCAGCAGCTAGACCTGAGCTGGTGAAGCCTGGGCTTCAGTGAAGATA 343
Qy 61 TCCTGCAAGCTTCCTGTTACTCATTCACCTGGCTACTACATGCATCGGCTGAGCAGAGC 120
Db 344 TCCTGCAAGCTTCCTGTTACTCATTCACCTGGCTACTACATGCATCGGCTGAGCAGAGC 403
Qy 121 CATGGAAGAGCCTTCAGTGGATTGACGTATTAATCCTTAAGCAATGGTGTACTCTCTAC 180
Db 404 CATGGAAGAGCCTTCAGTGGATTGACGTATTAATCCTTAAGCAATGGTGTACTCTCTAC 463
Qy 181 AACCGAAATTCAGGACCAAGGCATATTAAGTGTAGACAAGTCATCCACACAGCCTAC 240
Db 464 AACCGAAATTCAGGACCAAGGCATATTAAGTGTAGACAAGTCATCCACACAGCCTAC 523
Qy 241 ATGGAGCTCCGACGCTGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 294
Db 524 ATGGAGCTCCGACGCTGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 577

RESULT 15
BF577847
LOCUS
DEFINITION
602092155F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4206540 5',
mRNA sequence.
ACCESSION
BF577847
VERSION
BF577847.1 GI:11651559
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 684)

AUTHORS
TITLE
JOURNAL
COMMENT
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLN9767 row: n column: 13
High quality sequence stop: 672.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:4206540"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: oligo dt.
Average insert size 1.6 Kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 35.8%; Score 261; DB 2; Length 684;
Best Local Similarity 85.0%; Pred. No. 1.9e-67;
Matches 307; Conservative 0; Mismatches 45; Indels 9; Gaps 1;
Qy 1 GAGGTCAGCTTCAGCAGCTGCGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 60
Db 55 GAGGTCAGCTGCAGCAGCTGCGACCTGAGCTGGTGAAGCCTGGGCTTCAGTGAAGATG 114
Qy 61 TCCTGCAAGCTTCCTGTTACTCATTCACCTGGCTACTACATGCATCGGCTGAGCAGAGC 120
Db 115 TCCTGCAAGCTTCCTGTTACTCATTCACCTGGCTACTACATGCATCGGCTGAGCAGAGC 174
Qy 121 CATGGAAGAGCCTTCAGTGGATTGACGTATTAATCCTTAAGCAATGGTGTACTCTCTAC 180
Db 175 CATGGAAGAGCCTTCAGTGGATTGACGTATTAATCCTTAAGCAATGGTGTACTCTCTAC 234
Qy 181 AACCGAAATTCAGGACCAAGGCATATTAAGTGTAGACAAGTCATCCACACAGCCTAC 240
Db 235 AACCGAAATTCAGGACCAAGGCATATTAAGTGTAGACAAGTCATCCACACAGCCTAC 294
Qy 241 ATGGAGCTCCGACGCTGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
Db 295 ATGGAGCTCCGACGCTGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGACTTT 354
Qy 301 ATGATTACGAATCTGTTATGAGACTCTGGGTCAAGTAACTCAGTCAACCTCAGTCAACCTCTCTCA 360
Db 355 GGTA-----ACTACGGGAGACTACTCGGGTCAAGGAACCTCAGTCAACCTCTCTCTCA 405
Qy 361 G 361
Db 406 G 406

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